



**FIGURE 1**

CTAAAAAAATATGTTCTCTACAACACCAAGGCTCATTAAAATATTTAAATATT  
AATATACATTTCTCTGTCAAGAAATACATAAAACTTTATTATATCAGCGCAGG  
GCAGCGCGCCGCGTCGGTCCGGAGCAGAACCCGGCTTTCTGGAGCGACG  
CTGTCCTAGTCGCTGATCCCAAATGCAACCGGCTCATCTTGTCACACTCTA  
ATCTGCGCAAACCTTGCAGCTGTCGGACACTTCTGAACCCCGCAGAGCG  
CATCCATCAAAGCTTGCGLAACGCCAACCTCAGGCAGAGTGAGAGCAATCA  
CCTCACAGACTTGTACCGAAGAGATGAGACCATCCAGGTGAAGGAAACCG  
CTACGTGCAAGAGTCTAGATTCGGACAGCTACCCCAGGAACCTGCTCCTG  
ACATGGCGGCTTCACTCTCAGGAGAATACAGGATACAGTAGTGTGTTGACA  
ATCAGTTGGATTAGAGGAAGCAGAAAATGATATCTGTTAGGTATGTTTGT  
GGAAGTTGAAGATATTCGAACACAGTACCAATTAGAGGACGATGGTGT  
GGACACAAGGAAGTTCTCCAAGGATAAAATCAAGAACGAACCAAAATTAAA  
ATCACATTCAAGTCGATGACTACTTGTGGCTAACCTGGATTCAAGATTAA  
TTATTCTTGTGGAAGATTTCAACCCGCAAGCAGCTTCAGAGACCAACTGGG  
AATCTGTACAAGCTCTATTCAAGGGTATCTATAACTCTCCATCAGTAACG  
GATCCCACTCTGATTGCGGATGCTCTGGACAAAAAAATGCAAGAATTGATA  
CAGTGGAGAATCTGTCAGACTTCAATCAGAGTCATGGCAAGAAGATCT  
TGAGAATATGATCTGGACACCCCTCGGTATCGAGGGCAGGTACATCCATGAC  
CGGAAGTCAAAAGTTGACCTGGTAGGCTCAATGATGATGCCAACGCTTACA  
GTTGCACTCCAGGAATTACTCGGTCAATATAAGAGAACAGCTGAAGTTGGC  
CAATGTGGTCTCTTCCACGTTGCGCTCTCGTCAGCAGCTGTGGAGGAAATT  
GTGGCTGTGGAACTGTCACAGGAGGTCTGCACATGCAATTCAAGGAAAAC  
CGTAAAAAAAGTATCATGAGGTATTACAGTTGAGCCTGCCACATCAAGAGG  
AGGGTAGAGCTAACGACCATGGCTAGTTGACATCCAGTTGGATCACCAGT  
AACGATGTGATTGATCTGCAAGCTCAAGACCCACTCGATAAGAGAACATGTGCA  
CATCTTACATTAAAGCCTGAAGAACCTTGTATAAGGAGGGTGAGATAAG  
AGACCCCTTCTCCTACAGCAACCAAACCTACTACTAGCCTGAATGCAATGA  
ACACAAGTGGTTGCTGAGTCTCAGCCTTGTGTTAATGCCATGGCAAGTAG  
AAAGGTATATCATCAACTTCTACCTAACGAAATAGGATTGCAATTAAAT  
AGTGGTTGAGGTATATGCAACAAACACAGAAAATATATTCTGTCAT  
GTGTTGAGGTATATGCAATGTTTTGGTATATATAACCAAGGTACACCAGAGC  
TTACATATGTTGAGTTAGACTCTAAATCCTTGTGCAAAATAAGGGATGGT  
CAAATATATGAAACATGCTTTAGAAAATTAGGAGATAAATTATTTTAAA  
TTTGTGAAACACAAAACAATTGAAATCTGCTCTTAAAGAAAGCATCTGT  
ATATTAAAAATCAAAGATGAGGCTTCTACATATACATCTTAGTTG (SEQ  
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Figure 2A

1 CTAAGAAATATGTCCTACAAACACCAAGGCTCATTAATAATTATT  
46 TAAATATTAATATACATTCTCTCTGTCAGAAATACATAAAACTT  
91 ATTATATCAGCGCAGCGCGCGCGCTCGTCCGGAGCAGAA  
136 CCGCGCTTTCTGGAGCGACGCTGTCTCTAGTCGCTGATCCCA  
  
181 AATGCACCGGCTCATCTTGTCTACACTCTAATCTGCCAAACTT  
MetHisArgLeuIlePheValTyrThrLeuIleCysAlaAsnPhe  
10  
226 TTGCAGCTGTCGGGACACTTCTGCAACCCCGCAGAGCGCATCCAT  
CysSerCysArgAspThrSerAlaThrProGlnSerAlaSerIle  
  
271 CAAAGCTTGCGCACGCCAACCTCAGGGAGATGAGAGCAATCA  
LysAlaLeuArgAsnAlaAsnLeuArgArgAspGluSerAsnHis  
15  
  
316 CCTCACAGACTGTGACCGAAGGAGATGAGACCATCCAGGTGAAAGG  
LeuThrAspLeuTyrArgArgAspGluThrIleGlnValLysGly  
  
20 361 AAAACOGCTACGTCAGACTCTCTAGATTCGGAACAGCTACCCAG  
AsnGlyTyrValGlnSerProArgPheProAsnSerTyrProArg  
  
406 GAACTCTGCTCTGACATGGCGCGCTCACCTCTCAGGAGAAATACACG  
AsnLeuLeuLeuThrTrpArgLeuHisSerGlnGluAsnThrArg  
25  
451 GATACAGCTAGTGTGACAATCAGTTGGATTAGAGGAAGCAGA  
IleGlnLeuValPheAspAsnGlnPheGlyLeuGluGluAlaGlu  
  
496 AAAATGATATCTGTAAGGATATGATTTGTGGAAGTTGAAGATATAC  
AsnAspIleCysArgThrAspPheValGluValGluAspIleSer  
  
541 CGAAACCACTGACCATATTATTAGAGGACGATGGTGGACACAAGGA  
GluThrSerThrIleArgGlyArgTrpCysGlyHisIleGlu  
  
30  
586 AGTTCCTCCAGGATAAAATCAAGAACGAAACCAAAATTAAAATCAC  
ValProProArgIleIleSerArgThrAsnGlnIleIleGluThr  
  
631 ATTCAAGTCCGATGACTACTTGTGGCTAAACCTGGATTCAAGAT



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Figure 2B

PheLysSerAspAspTyrPheValAlaLysProGlyPheLysIle

676 TTATATTCTTGCTGGAAAGATTTCAAACCCGAGCAGCTTCAGA  
TyrTyrSerLeuLeuGluAspPheGlnProAlaAlaSerGlu

721 GACCAACTGGAAATCTGTACAAAGCTCTATTCAGGGGTATCCTA  
ThrAsnTrpGluSerValThrSerSerIleSerGlyValSerTyr

766 TAATCTCCATCAGTAACGGATCCCACCTGATTGCGGATGCTCT  
AsnSerProSerValThrAspProThrLeuIleAlaAspAlaLeu

811 GGACAAAAAAATTGCAGAATTGATACTAGTGGAAAGATCTGGCTCAA  
AspLysLysIleAlaGluPheAspThrValGluAspLeuLeuLys

856 GTACTTCAATCCAGAGTCATGGCAAGAAAGATCTTGAGAATATGTA  
TyrPheAsnProGluSerTrpGlnGluAspLeuGluAsnMetTyr

901 TCTGGCACCCCCCTCGGTATCGAGGCAGGTCAATCCATGACCGGAA  
LeuAspThrProArgTyrArgGlyArgSerTyrHisAspArgLys

946 GTCAAAAGTTGACCTGGATAGGCTCAATGATGATGCCAAGGGTTA  
SerLysValAspLeuAspArgLeuAsnAspAspAlaLysArgTyr

991 CAGTTTCACTCCCAGGAATTACTCGTCAATATAAGAGAACAGCT  
SerCysThrProArgAsnTyrSerValAsnIleArgGluGluLeu

1036 GAAGTTGGCCAAATGTGGCTCTCTTCCACGGTGCCTCTCGTGCA  
LysLeuAlaAsnValValPhePheProArgCysLeuLeuValGln

1081 GCGCTGTGGAGGAAATTGTGGCTGTGGAAACTGTCAACTGGAGGTC  
ArgCysGlyGlyAsnCysGlyCysGlyThrValAsnTrpArgSer

1126 CTGCAACATGCAATTCAAGGAAACCGTGAAGAAAGTATCATGAGGT  
CysThrCysAsnSerGlyLysThrValLysLysTyrHisGluVal

1171 ATTACAGTTGAGGCCACATCAAGAGGAGGGGTAGAGCTAA  
LeuGlnPheGluProGlyHisIleLysArgArgGlyArgAlaLys



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1216 GACCATGGCTCTAGTTGACATCCAGTGGATCACCATGAACGATG  
ThrMetAlaLeuValAspIleGlnLeuAspHisHisGluArgCys

Figure 2C

5 1261 TGATTGTATCTGCAGCTCAAGACCACCTCGATAAGAGATGTGCA  
AspCysIleCysSerSerArgProProArg (SEQ ID NO:12)

1306 CATCCTTACATTAGCCTGAAAGAACCTTTAGTTAAGGAGGGTG

1351 AGATAAGAGAACCTTTCTACAGCAACCAAACCTACTACTAGC

1396 CTGCAATGCAATGAACACAAAGTGTTGCTGAGTCCTCAGCCTTGGCT

10 1441 TTGTTAATGCCATGGCAAGTAGAAAAGGTATATCATCAACTCTAT

1486 ACCTAAGAATATAGGATTGCAATTAAATTAATAGTGTTGAGGTAT

1531 ATATGCACAAACACACACAGAAAATATATTCTATGTCTATGTTATA

1576 TAGATCAAATGTTTTTTGGTATATATAACCCAGGTACACCAGAG

1621 CTTACATATGTTGAGTTAGACTCTTAAATCCTTGCACAAATA

1666 AGGGATGGTCAAATATATGAAACATGTCCTTAGAAAATTTAGGAG

1711 ATAAAATTATTTTAAATTTTGAAACACAAAACAATTGGAAATCT

1756 TGCTCTCTAAAGAAAGCATCTGTATATAAAAATCAAAAGATG

1801 AGGCTTCTTACATACATACATCTTAGTTG (SEQ ID NO:50)



FIGURE 3

A -- Cur2 1.6 heavy chain nucleotide sequence

GAGGTGCAGCTGGAGTCTGGGGAGGCCCTGGTCAAGCCTGGGGGGTCCC  
TGAGACTCTCTGTGCAGCCTCTGGATTCAACTTCAGAACCTATAACATGAAC  
TGGGTCCGCCAGGCTCAGGGAAGGGCTGGAGTGGGTCTCATCCATTAGTA  
GTAGTAGTAGTAACTATACAGCAGACTCAGTGAAGGGCCGATTACCAT  
CTCCAGAGACACGCCAAGAACACTCACTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTATAATTACTGTGCGAGAGATATTATGATTACGTTG  
GGGAAATTATCGCCTCGTCACTTGTACTACTGGGGCCAGGGAACCCCTGGTC  
ACCGTCTCTCAG (SEQ ID NO:55)

B -- Cur2 1.6 heavy chain amino acid sequence

EVQLVESGGGLVKGPGSLRLSCAASGFNFRTYNMNWVRQAPGKGLEWVSSISSS  
SSNIYIADSVKGRTISRDNAKNSLYLQMNSLRAEDTAVYYCARDIMITFGGIAS  
FYFDYWGQGTLVTVVSS (SEQ ID NO:13)

C -- Cur2 1.6 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTGCCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TTTCAGCAGAAAACCAGGGAAAGCCCCTAAGGCCCTGATCTATGCTGCATCCA  
GTTTGCAGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGACAGA  
ATTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCGCTACTTCGGCGAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:56)

D -- Cur2 1.6 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGFQQKPGKAPKR<sub>L</sub>IYAASSLQ  
SGVP<sub>S</sub>RFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGT<sub>K</sub>VEIK (SEQ  
ID NO:14)



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FIGURE 4

A -- Cur2 1.11 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCAGGAGGCTTGATCCAGCCTGGGGGTCCC  
TGAGACTCTCTGTGCAGCCTCTGGGTTCACCGTCAGTAGCAACTACATGAGC  
TGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGTTATTATA  
GCGGTGGTAGCACATACTACCGCAGACTCCGTGAAGGGCCATTACCATCTC  
CAGAGACAATTCCAAGAACACCGCTGTATCTTCAAATGAACAGCCTGAGAGCC  
GAGGACACGGCCGTATTACTGTGCGGGAACGGTGAACGAATTACTACT  
ACGGTATGGACGTCTGGGGCAAGGGACCACGGTCACCGTCTCCTCAG (SEQ  
ID NO:57)

B -- Cur2 1.11 heavy chain amino acid sequence

EVQLVQSGGLIQPGLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVIYSG  
GSTYYADSVKGFRFTISRDNSKNLTYLQMNSLRAEDTAVYYCAGTVTTNYYGM  
DVWGQGTTVTVSS (SEQ ID NO:15)

C -- Cur2 1.11 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC  
GGCCTCATCTCTGCAGGTCTAGTCAGAGCCTCTGCAAAGTAATGGATAC  
AACTATTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGA  
TCTATTGGGTTCTAATCGGGCCTCCGGGTCCCTGACAGGTTCAGTGGCAGT  
GGATCAGGCACAGATTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATG  
TTGGGGTTTATTACTGCATGCAAGCTCACAAACTCTCACTTCGGCGGAGGG  
ACCAAGGTGGAGATCAAAC (SEQ ID NO:58)

D -- Cur2 1.11 light chain amino acid sequence

DIVMTQSPLSLPVTPGEPAISCRSSQSLQSNGYNLDWYLQKPGQSPQLLIYG  
SNRASGPDRFSGSGTDFTLKISRVEAEDVGVYYCMQALQTLFGGGTKVEI  
K (SEQ ID NO:16)

**FIGURE 5**

A -- Cur2 1.17 heavy chain nucleotide sequence

CAGGTGCAGCTGGGGAGCGCTGGTCCAGCCTGGGAAGTCCTGGAGACTCTCTGTGCAGCGTCTGGATTACCTTCAGTAGCTATGGCATGCAC  
TGGTCCGCCAGGCTCCAGGCAGGGCTGGAGTGGGTGGCAGTTATATGGT  
ATGATGGAAGTAATAAACTATGCAGACTCCGTGAAGGGCCGATTACCAT  
CTCCAGAGACAATCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTATTACTGTGCGAGAGATCAAGGATACAGATATG  
CTGGTTACTACTACGACTACGGTATGGACCTGGGGCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:59)

B -- Cur2 1.17 heavy chain protein sequence

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIW  
YDGSNKYYADSVKGRTFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYA  
GYYDYGMDVWGQGTVTVSS (SEQ ID NO:17)

C -- Cur2 1.17 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCCAGGGAAAGCCCCATAAGGTTCAAGCGCTGATCTATGCTGCATCCA  
GTTTGCAAAGTGGGTCCCATAAGGTTCAAGCGCTGAGCTGGATCTGGGACAGA  
ATTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTAACT  
GTCTACAGCATAATAGTTACCCGCTACTTCGGCGAGGGACCAAGGTGGA  
GATCAAAC (SEQ ID NO:60)

D -- Cur2 1.17 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPLTFGGGTKEIK (SEQ  
ID NO:18)



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FIGURE 6

A -- Cur2 1.18 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAACGCTGGGCCCTCA  
GTGAAGGTCTCTGCAAGGCTCTGGATACACCTTCACCGATTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCAACAGTGGTAACACAGGCTATGCACAGAACAGTTCAAGGGCAGAGTCACC  
ATGACCAAGGAAACACCTCCATAAGCACAGCTACATGGAGCTGAGCACCTGA  
GATCTGAGGACACGGCCGTGATTACTGTGCGAGAGAGGGTATAGCAGTGGC  
TGGGACATACTACTACTACCGTATGGACGTCTGGGCCAAGGGACCACG  
GTCACCGTCTCTCAG (SEQ ID NO:61)

B -- Cur2 1.18 heavy chain protein sequence

QVQLVQSGAEVKPGAVSVKSKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDATAVYYCAREGIAVAG  
YYYYYYGMDVWGQGTTVTVSS (SEQ D NO:19)

C -- Cur2 1.18 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCATGCTGATCTGAGGAGACAG  
AGTCACCATCACTTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCCAGGGAAAGCCCCATAAGCCCTGATCTATGTCATCCA  
GTTGCAAAGTGGGTCCCATAAGGTTCAAGCGGCAGTGGATCTGGACAGA  
ATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTCT  
GTCTACAGCATAATAGTTACCCATTCACTTCGGCCCTGGGACCAAAGTGGAT  
ATCAAAC (SEQ ID NO:62)

D -- Cur2 1.18 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRIYAASSLQ  
SGVPSRFSGSGSTEFTLTISSLQPEDFATYFCLQHNSYPFTFGPGTKVDIK (SEQ  
ID NO:20)



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FIGURE 7

A -- Cur2 1.19 heavy chain nucleotide sequence

CAGGTGCAGCTGGTCAGTCTGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCGATTATGATATCAC  
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAAC  
CCTAACAGTGGTAACACAGGCTATGCACAGAACAGTTCCAGGGCAGAGTCACCA  
TGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAG  
ATCTGAGGACACGGCGTGTATTACTGTGCGAGAGACGTTATGATTACGTTTG  
GGGGAGTTATCGTGCACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:63)

B -- Cur2 1.19 heavy chain amino acid sequence

QVQLVQSGAEVKPGAVKVSKASGYTFSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDVMITFG  
GVIVHYGMDVWGQGTTVTVSS (SEQ ID NO:21)

C -- Cur2 1.19 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCCAGGGAAAGCCCCTAAGCCCTGATCTATGCTGCATCCA  
GTTTCAAAGTGGGTCCCCTCAAGGTTCAGCGGCAGTGGATCTGGACAGA  
TTTCACTCTACAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTGACCCGTGCAGTTGGCCAGGGGACCAAGCTGGA  
GATCAGAC (SEQ ID NO:64)

D -- Cur2 1.19 light chain amino acid sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRIYAASSLQ  
SGVPSRFSGSGSGTDFLTISSLQPEDFATYYCLQHNSDPCSFQGTKLEIR (SEQ  
ID NO:22)



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**FIGURE 8**

A -- Cur2 1.23 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTGAAGATCCTGTGAGGGTTCTGGATACAGCTTACAGCTACTGGATCGGCTGGGTGCGCCAGATGCCCGGGAAAGGCCCTGGAGTGGAATGGGATCATCTATCCTGGTGA C T G A T A C C A G A T A C G C A C C G C T A C C T G C A G T G G A G C A G C C T G A A G G C T C A C C G C A C C G C A C T G A T T A C T G T G C G A G A C T G T A T C G T A T T A C T A T G T T T C G G G A G T T A T T A A C G T C T T G A C T A C T G G G G C C A G G G A A C C T G G T C A C C G T C C T C A G (SEQ ID NO:65)

B -- Cur2 1.23 heavy chain amino acid sequence

EVQLVQSGAEVKKPGESELKISCEGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGVQTISADKSISTAYLQWSSLKASDTAMYYCARHVSYYYYVSGS  
YYNVFDYWGQGTLTVSS (SEQ ID NO:23)

C -- Cur2 1.23 light chain nucleotide sequence

GACATCCAGATGCCAGTCTCCATCCTCCCTGTCTGCATCTTAGGAGACAG  
AGTCACCATCACTGCCGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGATACCAGGGAAAGCCCCTAACGCCCTGATCTATGCTGCATCCA  
GTTTGCAACGTGGGTCCCATCAAGGTTCACGCCAGCAGCTGAAGATTGCAACTTATTACT  
ATTCACTCTCACAAATCAGCACGCCCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCGTGGACGTTCGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:66)

D -- Cur2 1.23 light chain amino acid sequence

DIQMKTQSPSSLASVGDRVTITCRASQGIRNDLGWYQQIPGKAPKRLIYAASSLQR  
GVPSRFSGSGSTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:24)



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FIGURE 9

A -- Cur2 1.24.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCC  
TGAGACTCTCGTGCAGCGTCTGGATTCAAGTTTCAGTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGAAGGGCTGGAGTGGGTGGCAGATATATGGT  
ATGATGGAAGTAATAAAACTATGCAGACTCCGTGAAGGGCCGATTACCAT  
CTCCAGAGACAATCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCGGAGGACACGGCTGTGTATTATGTGCGAGAGATCAGGGATACAGCTATG  
GTTACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGT  
CACCGTCTCCTCAG (SEQ ID NO:67)

B -- Cur2 1.24.1 heavy chain protein sequence

QVQLVESGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIW  
YDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYSYG  
YVYYDYGMVDWGQQTTVTVSS (SEQ ID NO:25)

C -- Cur2 1.24.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCATAAGGGCTGATCTATGCTGATCCA  
GTTGCAAAGTGGGTCCCATAAGGTTCAAGGTTCAAGGCTGAGCTGGATCTGGGACAGA  
GTTCACTCTCACAAATCAGCAGCCTGCAGCCTGAAGATTGCAACTTAACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:68)

D -- Cur2 1.24.1 light chain protein sequence

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQ  
SGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:26)



FIGURE 10

A -- Cur2 1.25.1 heavy chain nucleotide sequence

GAGGTGAGCTGGTCAGTCGGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTTCTGGATACAGGTTACAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTGACTCTGATACCAGATAACAGCCCTCCTCCAAGGCCAGGTACCA  
TCTCAGCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCCCATGTATTACTGTGCGAGACATGGATCGTATTATTATG  
GTTCCGGAGACTTATTATAATGTTGACTACTGGGCCAGGGAACCCCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:69)

B -- Cur2 1.25.1 heavy chain protein sequence

EVQLVQSGAEVKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHGSYYYGSET  
YYNVFDYWQGQTLTVVSS (SEQ ID NO:27)

C -- Cur2 1.25.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCATCCTCCCTGTCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAAACCAGGGAAAGCCCCTAAGGCCCTGATCTATGCTCATCCA  
GTTTGCAAAGTGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGACAGA  
ATTCACTCTCACATCAGCACGCTGCAGCCTGAAGATTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCCGTGGACGTTGGCCAAGGGACCAAGGTGGA  
AATCAAAC (SEQ ID NO:70)

D -- Cur2 1.25.1 light chain protein sequence

DIQMTQSPSSLASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRIYAASSLQ  
SGVPSRFSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFQGQTKVEIK (SEQ  
ID NO:28)



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**FIGURE 11**

A -- Cur2 1.29 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCAGAGGTAAAAAGCCCGGGAGTCT  
CTGAAGATCTCTGTAAGGGTCTGGATACAGCTTACAGCTACTGGATCGG  
CTGGTGCAGATGCCGGAAAGGCCTGGAGTGGATGGGATCATCTAT  
CCTGGTACTCTGATACCAGATAACAGCCCTCCTCCAAGGCCAGGCCACCA  
TCTCAGCCACAAGTCCATCAGCACCGCCTACCTGCACTGGAGCAGCTGAA  
GCCCTGGACACGCCATGTATTACTGTGCGAGACACGTGGATGTAGGGCT  
ACGATTGGGATATTACTATTACTACACCGGTATGGACGTCTGGGGCCAAG  
GGACACGGTCACCGTCTCCTAG (SEQ ID NO:71)

B -- Cur2 1.29 heavy chain protein sequence

EVQLVQSGAEVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDTRYSPSFQGQATISADKSISTAYLQWSSLKASDTAMYCARHVDVGATIGG  
YYYYYHGMDDVVWGQGTTVTVSS (SEQ ID NO:29)

C -- Cur2 1.29 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC  
GGCCTCCATCTCTGCAAGGTCTAGTCAGAGCCTCTGCATAGTAATGGATACA  
ACTATTTGGATTGGTACCTGCAAGAACGCCAGGGCAGTCTCCACAACTCTGATC  
TATTGGGTTCTAATCGGGCTCCGGGCTCTGACAGGTTCACTGGCAGTGG  
ATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGACGATGTT  
GGGGTTTATTACTGCATGCAAGCTCTACAACTCTCATGTGCAGTTGGCCA  
GGGGACCAAGCTGGAGATCAAAC (SEQ ID NO:72)

D -- Cur2 1.29 light chain protein sequence

DIVMTQSPLSLPVTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPQLIYLG  
SNRASGVPDFRGSGSGTDFTLKISRVEADDVGVYYCMQALQSLMCSFGQGTKL  
EIK (SEQ ID NO:30)



FIGURE 12

A -- Cur2 1.33 heavy chain nucleotide sequence

CAGGTTCAGCTGGTGCAGTCGGGAGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCTGCAAGGCTCTGGTTACACCTTACCACTATGGTATCAGC  
TGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG  
CTTACAATGGTAACACAAACTATGACACAGAAGCTCCAGGGCAGAGTCACCAT  
GACCACAGACACATCCACGACAGCAGCCTACATGGAGCTGAGGAGCCTGAG  
ATCTGACGACACGGCGTGTATTACTGTGGAGAGATCATTACTATGATAGT  
AGTGATTATCTCTACTACTACGGTTGGACGTCTGGGCCAAGGGACCAC  
GGTCACCGTCTCTCAG (SEQ ID NO:73)

B -- Cur2 1.33 heavy chain protein sequence

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA  
YNGNTNYAQKLQGRVTMTDTSTAYMELRSLSRSDDTAVYYCARDHYDSS  
DYLYYYYGLDVWGQGTTVTVSS (SEQ ID NO:31)

C -- Cur2 1.33 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCTGGGGAGTCAGGGCATTAGCAATTATTAGCCTGGT  
ATCAGCAGAACCAACAGGGAAAGTCTCAAGCTCTGATCTATGCTGCATCCAC  
TTTGAATCAGGGTCCCCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATT  
TCACTTCACCATCAGCAGCTGCAGCCTGAAGATGTTGCAACTTATTACTGT  
CAAAGTATAACAGTGGCCCCCTCACTTCCGGCGAGGGACCAAGGTGGAGA  
TCAAAC (SEQ ID NO:74)

D -- Cur2 1.33 light chain protein sequence

DIQMTQPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTLQ  
SGVPSRFSGSGTDFLTISLQPEDVATYYCQKYNSAPLTFGGGTKVEIK (SEQ  
ID NO:32)



FIGURE 13

A -- Cur2 1.38.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGGAGTCGGGGGGAGCGTGGTCCAGCCTGGGAGGTCCC  
TGAGACTCTCCTGTGCAGCGCTGGATTACACCTTCAGTAGCTATGGCATGCAC  
TGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGTGGCAATTATATGGT  
ATGATGGAATGATAAAATACTATGCAGACTCCGTGAAGGGCCGCTCACCGT  
CTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA  
GCCGAGGACACGGCTGTGTTACTGTGCGAGAGGATATTACTATGATAGTA  
GTGATTATCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCAC  
GGTCACCGTCTCTCAG (SEQ ID NO:75)

B -- Cur2 1.38.1 heavy chain protein sequence

QVQLVESGGVVQPGRSLRLSCAASGFTSSYGMHWVRQAPGKGLEWVAIIWY  
DGNDKYYADSVKGRFTVSRDNSKNTLYLQMNSLRAEDTAVYYCARGYYYDSS  
DYLYYYYYGMDVWGQGTVTVSS (SEQ ID NO:33)

C -- Cur2 1.38.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAG  
AGTCACCATCACTTGGCCGGGGAGTCAGGGCATTAGCAATTATTTAGCCTGGT  
ATCAGCAGAAACCAGGGAAAGTTCCAACCTCCTGATCTATGCTGCATCCAC  
TTTGAATCAGGGGTCCTCATCTGGTTCACTGGCAGTGGATCTGGGACAGATT  
TCTCTCTACCACATCAGCAGCCTGCAGCCTGAAGATGTTGAGCTTATTACTGT  
CAAAGTGTAAACAGTGCCCCGGACGTTGGCCAAAGGGACCACGGTGGAG  
ATCAAAC (SEQ ID NO:76)

D -- Cur2 1.38.1 light chain protein sequence

DIQMTQSPSSLASVGDRVTITCRASQGISNYLAWYQQKPGKVPNLLIYAASTLQ  
SGVPSRFSGSGTDFSLTISSLQPEDVAAYCQKCNSAPWTFGQGTTVEIK (SEQ  
ID NO:34)



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**FIGURE 14**

A -- Cur2 1.39.1 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGAAACAGAGGTGAAAAAGCCGGGGAGTCT  
CTGAAGATCTCCTGTAAGGGTTCTGGATAACAGGTTACAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCGGGAAAGGCCCTGGAGTGGATGGGATCATCTAT  
CCTGGTACTCTGATACCAAGATAACAGCCGCTTACCTGCAGTGGAGCAGCCTGAA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA  
GGCCTCGGACACCGCCATGTATTACTGTGCGAGACATGGATCGTATTACTATA  
ATTGGGGAGTTATTATAACGTCTTGACTACTGGGCCAGGGAACCTGGTC  
ACCGTCTCCTCAG (SEQ ID NO:77)

B -- Cur2 1.39.1 heavy chain protein sequence

EVQLVQSGTEVKPGESLKISKCGSGYRFTSYWIGWVRQMPGKGLEWMGIYYPG  
DSDTRYSPSFQQVTISADKSISTAYLQWSSLKASDTAMYCARHGSYYNSGS  
YYNVFDYWQGTLTVSS (SEQ ID NO:35)

C -- Cur2 1.39.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCAGTCATCTGTAGGAGACAG  
AGTCACCATCACTTGCCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATCCA  
GTTTCAAAGTGGGGTCCCATAAGGTTCAAGCGCAGTGGATCTGGACAGA  
ATTCACTCTACAATCAGCACCGCTGCAGCCTGAAGATTTGCAACTTATTACT  
GTCTACAGCATAATAGTTACCGTGGACGTTCGGCCAGGGACCAAGGGTGA  
AATCAAAC (SEQ ID NO:78)

D -- Cur2 1.39.1 light chain protein sequence

DIQMTOQPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRRIYAASSLQ  
SGVPSPRGSGSGTEFTLTISSLQPEDFATYYCLQHNSYPWTFGQGTKVEIK (SEQ  
ID NO:36)

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**FIGURE 15**

A -- Cur2 1.40.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTCAGTCGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA  
GTGAAGGTCTCTGCAAGGCTCTGGATAACCTTCACCACTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATGAA  
CCCTAACAGTGGTAACACAGGCTATGCACAGAAGTTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCCTAACGACACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCGTGTATTACTGTGCGAGAGATATTGAGTGGTGGT  
AGCTGCTACCAACTACTACAAACGGTATGGACGTCTGGGGCCAAGGGACACG  
GTCACCGTCTCCTCAG (SEQ ID NO:79)

B -- Cur2 1.40.1 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFITDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSLSTAYMELSSLRSEDTAVYYCARDIVVVV  
AATNYYNGMDVWGQGTTVTVSS (SEQ ID NO:37)



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FIGURE 16

A -- Cur2 1.45 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAACGCTGGGGCTCA  
GTGAAGGTCTCTGCAAGGCTCTGGATACACCTTCACCAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGATGGATGGATGAA  
CCCTAACAGTGGTAACACAGGCTATGCACAGAACAGTCCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCGTGTATTACTGTGCGAGAGGCAGTGGATACAGCTA  
TGGTTACGACTACTACTACGGTACGGTACGGTCTGGGGCCAAGGGACCACGGTC  
ACCGTCTCCTCAG (SEQ ID NO:80)

B -- Cur2 1.45 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGWM  
NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARGSGYSYG  
YDYYYGMDVWGQGTTVTVSS (SEQ ID NO:38)

C -- Cur2 1.45 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGGAGACAG  
AGTCACCATCAATTGCCGGGAGTCAGGGCATTAGCAATGATTAGCCTGG  
TATCAGCAGAAAACCAGGGAAAGTTCTAACGCTCTGATCTATGCTGCATCCA  
CTTGCAATTAGGGGTCCTCTCGGTTCACTGGCAGTGGATCTGGACAGAT  
TTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTG  
TCAAAAGTATAACAGTGCCCCATTCACTTCGGCCCTGGGACCAAAAGTGGAT  
ATCAAAC (SEQ ID NO:81)

D -- Cur2 1.45 light chain protein sequence

DIQMTPSPSSLSASVGDRVTINCRASQGISNDLAWYQQKPGKVPKLLIYAASTLQ  
LGVPSRFSGSGSGTDFTLTISLQPEDVATYYCQKYNSAPFTFGPGTKVDIK (SEQ  
ID NO:39)



FIGURE 17

A -- Cur2 1.46.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAACGCCCTGGGCCCTCA  
GTGAAGGTCTCCTGCAAGGCTTCTGGATACTCCTTCACCAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGAGATGGATGGATGAA  
CCCTAACAAATGTAACACAGGCTATGCACAGAACAGTTCCAGGGCAGAGTCACC  
ATGACCAAGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCGTGTATTACTGTGCGAGAGATATTGTAGTGGTGGT  
AACTGCTACGGACTACTACAGGTATGGACGTCTGGGCCAAGGGACCACG  
GTCACCGTCTCCTCAG (SEQ ID NO:82)

B -- Cur2 1.46.1 heavy chain protein sequence

QVQLVQSGAEVKPGASVKVSKASGYSFTSYDINWVRQATGQGLEWMGWM  
NPNNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARDIVVVVT  
ATDYYYYGMDVWGQGTTVTVVSS (SEQ ID NO:40)

C -- Cur2 1.46.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGAGACAG  
AGTCACCATCATTGCGGGCAAGTCAGGGCATTAGAAATGATTAGGCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAACGCCTGATTITGCTGCATCCA  
GTTTGCCAAGTGGGTCCCCTAACGGTTCAAGGTCAGCGGCAGTGGATCTGGGACAGA  
ATTCACTCTCACAACTCAGCAGCCTGCAGCCTGAAGATTTCGAACATTAACT  
GTCTACAGCATAAGTGGTACCCCTCGACGTTGGCCAAGGGACCAAGGGTGA  
AATCAAAC (SEQ ID NO:83)

D -- Cur2 1.46.1 light chain protein sequence

DIQMKTQSPSSLASAVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIFASSLPS  
GVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHSGYPPTFGQGTKVEIK (SEQ ID  
NO:41)

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FIGURE 18

A -- Cur2 1.48.1 heavy chain nucleotide sequence

CAGGTTCACTGGTGCAGTCGGGAGCTGAGGTGAAGAAAGCCTGGGGCCTCAG  
TGAAGGTCTCTGCAAGGCTCTGGTTACACCTTACAGCTATGGTATCAGC  
TGGTGCAGACAGGCCCTGGACAAGGGCTTGAGTGGATGGATGGATCAGCG  
CTTACAATGGTAACACAAACTATGCACAGAACGCTCCAGGGCAGAGTCACCAT  
GACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAGCCTGAG  
ATCTGACGACACGGCCGTATTACTGTGCGAGAGATGTTGAATATTACTATG  
ATGGTAGTGGTTATTACTACTTTGACTACTGGGCCAGGAAACCCTGGTCACC  
GTCTCCTCAG (SEQ ID NO:84)

B -- Cur2 1.48.1 heavy chain protein sequence

QVQLVQSGAEVKPKPGASVKSCKASGYTFTSYGISWVRQAPGQGLEWMGWISA  
YNGNTNYAQKLQGRVTMTDTSTAYMELRSLRSDDTAVYYCARDVEYYYD  
GSGYYYFDYWQGQTLTVSS (SEQ ID NO:42)

C -- Cur2 1.48.1 light chain nucleotide sequence

GACATCCAGATGACCCAGTCTCCATCTCCGTGTCATCTGTAGGGAGACAG  
AGTCACCATCACTTGTCCGGGAGTCAGGGTATTAGCAGCTGGTTAGCCTGG  
TATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCTGATCTATGCTGCATCCA  
TTTGCAAAGTGGGTCCCCATCAAGGTTCAAGCGGCAGCTGAGGATTTCATCTTACTATT  
TTTCACTCTCACCATCAGCAGCCTGCAGCCTGAGGATTTCATCTTACTATT  
GTCACAGTCTAACAGTTCCCTCGGACGTTCGGCCAAGGGACCAAGGGTGA  
GATCAAAC (SEQ ID NO:85)

D -- Cur2 1.48.1 light chain protein sequence

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYASILQ  
SGVPSRFSGSGSGTDFLTISLQPEDFASYYCQQNSFPRTFGQGTKVEIK (SEQ  
ID NO:43)



**FIGURE 19**

A -- Cur2 1.49.1 heavy chain nucleotide sequence

CAGGTGCAGCTGGTGCAGTCGGGGCTGAGGTGAAGAAGCCTGGGGCCTCA  
GTGAAGGTCTCTGCAAGGCTCTGGATACACCTCACAGTTATGATATCAA  
CTGGGTGCGACAGGCCACTGGACAAGGGCTGAGTGGATGGGATGGATGAA  
CCCTAACAGTGGTACACAGGCTATGCACAGAAGTTCAGGGCAGAGTCACC  
ATGACCAGGAACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGA  
GATCTGAGGACACGGCCGTGATTCTGTCGAGAATGAGGGATATAGTGGC  
TACGAGCTATTACTACTACTCTACGGTATGGACGTCTGGGGCCAAGGGACC  
ACGGTCACCGTCTCTCAG (SEQ ID NO:86)

B -- Cur2 1.49.1 heavy chain protein sequence

QVQLVQSGAEVKPKPGASVKVSCKASGYTFSYDINWVRQATGQGLEWMGW  
NPNSGDTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYFCARMRDIVAT  
SYYYYFYGMDVWVGQGTTTVSS (SEQ ID NO:44)

C -- Cur2 1.49.1 light chain nucleotide sequence

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCC  
GGCCTCCATCTCTGCAGGTCTAGTCAGAGCCTCTGCATAGTAATGGATACA  
ACTATTTGGATTGGTACCTGCTGAAGGCCAGGGCAGTCTCCACAGCTCCTGATC  
TATTGGGTTAGTCGGGCCCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGG  
ATCAGGCACAGATTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT  
GGGGTTTATTACTGCATGCAAACCTACAAACTATCACCTCGGCCAAGGGAA  
CACGACTGGAGATTAAC (SEQ ID NO:87)

D -- Cur2 1.49.1 light chain protein sequence

DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSNGYNLDWYLLKPGQSPQLIYLG  
SSRASGVPDFRGSGSGTDFTLKISRVEAEDVGYYCMQLTQTITFGQGTRLEIK  
(SEQ ID NO:45)



**FIGURE 20**

A -- Cur2 1.51 heavy chain nucleotide sequence

GAGGTGCAGCTGGTGCAGTCGGGAGCTGAGGTGAAAAAGCCCGGGAGTCT  
CTGAAGATCCTCTGAAGGGTCTGGATAACAGCTTACAGCTACTGGATCGG  
CTGGGTGCGCCAGATGCCCGGAAAGGCCCTGGAGTGGATGGGATCATCTAT  
CCTGGTGA~~C~~TGATGCCAAATACAGCCCGCTTCCAAGGCCAGGTCA  
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCTGAA  
GGCCTCGGACCCGCCATGTATTACTGTGCGAGACACTATGATTACGTTGGA  
GGAATTATCGGTATACAGGGTGGTICGACCCCTGGGCCAGGGAACCTGGT  
CACCGTCTCCAG (SEQ ID NO:88)

B -- Cur2 1.51.1 heavy chain protein sequence

EVQLVQSGAEVVKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIYPG  
DSDAKYSPSFQQQVTISADKSISTAYLQWSSLKASDTAMYYCARHYDYVWRNY  
RYTGWFDPWGQGTLTVTSS (SEQ ID NO:46)

C -- Cur2 1.51.1 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCGTCTTGTCTCCAGGGAAAG  
AGCCACCCCTCTCTGCAGGGCCAGTCAGAGTGTAGCAGCAGCTACTTAGCC  
TGGTACCCAGCAGAAACCTGGCCAGGCTCCAGGCTCCATCTATGGTGCAT  
CCAACAGGGCCACTGGCATCCCAGACAGGTTAGTGGCAGTGGGTCTGGGAC  
AGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTGAGTGTATT  
ACTGTCAGCAGTATGGTAGCTCACTATTCACTTCGGCCCTGGGACCAAAGTG  
GATATCAAAC (SEQ ID NO:89)

D -- Cur2 1.51.1 light chain protein sequence

EIVLTQSPGTLSSLSPGERATLSCRASQSVSSSYLA~~WY~~QQKPGQAPRLLIYGASNRA  
TGIPDRFSGSGSTDFTLTISRLEPEDFAVYYCQQYGSSLFTFGPGTKVDIK (SEQ  
ID NO:47)



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**FIGURE 21**

A -- Cur2 6.4 heavy chain nucleotide sequence

CAGGTGCAGCTGGTCAGTCGGGCTGAGGTGAAGAAGCCTGGGGCCTCAG  
TGAAGGTCTCCTGCAAGGCTCTGGATAACCTTCACCAGTTATGATATCAAC  
TGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGGATGGATAAAC  
CCTAATAGTGTAAACACAGACTATGCACAGAAGTCCAGGGCAGAGTCACCA  
TGACCAGGGACACCTCCATAAACGACAGCCTACATGGAGCTGAGCAGCCTGAG  
ATCTGAGGACACGGCATATATTATTGTGTGAGAGGCTTGGATAACAGCTAT  
AATTACGACTACTATTACGGTATGGACGTCTGGCCAAGGGACCACGGTCA  
CCGTCCTCAGT (SEQ ID NO:90)

B -- Cur2 6.4 heavy chain amino acid sequence

QVQLVQSGAEVKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMGWIN  
PNSGNTDYAQKFQGRVTMRTDSISTAYMELSSLRSEDTAIYYCVRGFGYSYNY  
DYYYGMDVWGQGTTVTVSS (SEQ ID NO:48)

C -- Cur2 6.4 light chain nucleotide sequence

GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTGCTTTGTCTCCAGGGGAAAG  
AGCCACCCCTCCTGCAAGGGCCAGTCAGAGTGTAGTAGTTACTAGCCT  
GGTACCAAGCAGAAGCCTGGCCAGGCTCCCAGGCTCCTCATCTATGCTACATC  
CAGCAGGGCCACTGGCATCCCAGACAGGTCAGTGGCAGTGGCTGGGACA  
GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTGCAGTGATT  
CTGTCAGCAGTATGGTAGTTCACCGTGCAGTTGGCCAGGGGACCAAGCTG  
GAAATCAAGC (SEQ ID NO:91)

D -- Cur2 6.4 light chain amino acid sequence

EIVLTQSPGTLSLPGERATLSCRASQSVSSSYLAWSQQKPGQAPRLLIYATSSRA  
TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSPPCSFGQGTLEIK (SEQ  
ID NO:49)

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FIGURE 22A

Clone	Germline genes used			No. of Nucleotide/ Amino acid changes						
	V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
	V	D	J	V					D & J	
CR2										
	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0
1.19.1	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/1
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0
	VK	mix								
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/1
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0
1.51.1	VH	S-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0

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Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

**FIGURE 22B**

Clone	Germline genes used			No. of Nucleotide/Amino acid changes						
	V	D	J	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
CR2						V				D & J
1.40.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0
	VK	mix								
1.48.1	VH	V1-18	D21-9	JH4B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	L5		JK1	0/0	0/0	0/0	1/1	2/1	1/1
1.49.1	VH	V1-8	D5-12	JH6B	1/0	0/0	0/0	1/1	1/1	0/0
	VK	A19		JK5	0/0	0/0	1/1	1/1	0/0	1/0
1.11.1	VH	V3-53	D4-17	JH6B	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A19		JK4	0/0	1/1	0/0	0/0	0/0	0/0
1.29	VH	V5-51	D5-12	JH6B	1/0	0/0	0/0	0/0	1/1	0/0
	VK	A19		JK2	0/0	0/0	1/0	0/0	1/1	0/0
1.45	VH	V1-8	DK4	JH6B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK3	1/1	1/1	0/0	1/1	0/0	0/0
1.33	VH	V1-18	D21-9	JH6B	1/0	0/0	0/0	0/0	0/0	0/0
	VK	A20		JK4	0/0	0/0	0/0	0/0	0/0	0/0
1.38.1	VH	V3-33	D21-9	JH6B	1/0	0/0	0/0	3/3	2/1	0/0
	VK	A20		JK1	0/0	0/0	1/1	0/0	2/2	1/1
6.4.1	VH	V1-8	D5-18	JH6B	0/0	0/0	0/0	3/2	5/3	0/0
	VK	A27		JK2	0/0	3/0	1/0	2/2	0/0	1/0
1.51.1	VH	S-51	D3-16	JH5B	2/0	0/0	0/0	1/1	1/1	0/0
	VK	A27		JK3	0/0	0/0	0/0	1/1	0/0	0/0
1.19.1	VH	V1-8	D3-16	JH6B	0/0	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK2	0/0	0/0	0/0	0/0	1/1	1/0
1.18	VH	V1-8	D6-19	JH6B	1/0	0/0	0/0	1/0	0/0	0/0
	VK	A30		JK3	0/0	0/0	0/0	0/0	1/1	0/0
1.6.1	VH	V3-21	D3-16	JH4B	0/0	4/4	0/0	1/1	1/0	0/0
	VK	A30		JK4	0/0	0/0	1/1	0/0	0/0	0/0
1.23.1	VH	V5-51	D3-10	JH4B	1/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	1/1	1/1	0/0	0/0
1.25.1	VH	V5-51	D3-10	JH4B	1/0	1/1	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0
1.39.1	VH	V5-51	D3-10	JH4B	2/1	1/1	0/0	0/0	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	0/0	0/0
1.17.1	VH	V3-33	D5-18	JH6B	2/1	0/0	0/0	0/0	0/0	0/0
	VK	A30		JK4	0/0	0/0	0/0	0/0	0/0	0/0
1.24.1	VH	V3-33	D5-18	JH6B	0/0	2/1	0/0	1/1	0/0	0/0
	VK	A30		JK1	0/0	0/0	0/0	0/0	1/0	0/0
1.46.1	VH	V1-8	D2	JH6B	1/0	1/1	0/0	0/0	1/1	0/0
	VK	A30		JK1	0/0	0/0	2/1	1/1	0/0	2/2

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Corvalan et al.  
Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 23A

Figure 23A

	(1)	10	20	30	40	50	Section 1
CUR2-1.61_HC	(1)	EVOLVEEGGGGLVKE	GBSLRLSCAASGF	NPF	YNNMNVROAPGKGLEWVSSI		
VH3-21	(1)	EVQLVESGGGGLVKD	GGBLRLESCAASGF	TFS	YMNWVROAPGKGLEWVSSI		
Consensus	(1)	EVQLVESGGGGLVKE	PGGSLRLSCAASGF	F	SY MNWVROAPGKGLEWVSSI		Section 2
	(52)	52	60	70	80	90	102
CUR2-1.61_HC	(52)	SSSSSSNITYYADSVR	GRAFTIERD	NARN	SYLYQMN	SLRAEDTAVYYCARDIMI	
VH3-21	(52)	SSSSSSNITYYADSVR	GRAFTIERD	NARN	SYLYQMN	SLRAEDTAVYYCAR	---
Consensus	(52)	SSSSSS	IYYADSVR	GRAFTISRD	NARN	SYLYQMN	SLRAEDTAVYYCAR
							Section 3
	(103)	103	110	120	126		
CUR2-1.61_HC	(103)	TFGGIIIA	SFYFDY	WGQGT	LVTVSS		
VH3-21	(99)	-----	-----	-----	-----		
Consensus	(103)						

Figure 23B

	(1)	10	20	30	40	50	Section 1
CUR2-1.61_LC	(1)	DIQMTQSPSPLASAVGDRVITCRASQGIRNDLGW	Q	QKPGKAPRRLIYAA			
A30	(1)	DIQMTQSPSPLASAVGDRVITCRASQGIRNDLGW	Q	QKPGKAPRRLIYAA			
Consensus	(1)	DIQMTQSPSPLASAVGDRVITCRASQGIRNDLGW	Q	QKPGKAPRRLIYAA			Section 2
	(52)	52	60	70	80	90	102
CUR2-1.61_LC	(52)	SSLCQGVPSRFGSGSGSGTEFTLTISL	Q	PEDFATYYC	LQHNSYP	ELTPGGGT	
A30	(52)	SSLCQGVPSRFGSGSGTEFTLTISL	Q	PEDFATYYC	LQHNSYP	-----	
Consensus	(52)	SSLCQGVPSRFGSGSGTEFTLTISL	Q	PEDFATYYC	LQHNSYP	-----	Section 3
	(103)	103	107				
CUR2-1.61_LC	(103)	KVEIK					
A30	(66)	-----					
Consensus	(103)						

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**FIGURE 24****Figure 24A**

	1	10	20	30	40	50	Section 1
Cur2-1.11.1 HC	(1)	EVLVBSGGGLIQPGGSRLSCAAAGFTVSSNYMSWVRQAPGRGLEWVSVI					
VB-53	(1)	EVLVBSGGGLIQPGGSRLSCAAAGFTVSSNYMSWVRQAPGRGLEWVSVI					
Consensus	(1)	EVLVBSGGGLIQPGGSRLSCAAAGFTVSSNYMSWVRQAPGRGLEWVSVI					Section 2
	(2)	52 60 70 80 90					102
Cur2-1.11.1_HC	(2)	YGGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAT					
VB-53	(2)	YGGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR					
Consensus	(2)	YGGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA					Section 3
	(103)	103 110 120					
Cur2-1.11.1_HC	(103)	YYGMDWVGCGTTTVSS					
VB-53	(96)	-----					
Consensus	(103)	-----					

**Figure 24B**

	1	10	20	30	40	50	Section 1
CUR2-1.11.1 LC	(1)	DIVMTQSPFLPLPVTPEPASISCRSSQSL					
A19	(1)	DIVMTQSPFLPLPVTPEPASISCRSSQSL					
Consensus	(1)	DIVMTQSPFLPLPVTPEPASISCRSSQSL					Section 2
	(2)	52 60 70 80 90					102
CUR2-1.11.1 LC	(2)	LIVLGNSRASGVDRFSGSGSGDFTLKISRVEAEVGVYYCMQALCP-TF					
A19	(2)	LIVLGNSRASGVDRFSGSGSGDFTLKISRVEAEVGVYYCMQALCP-TF					
Consensus	(2)	LIVLGNSRASGVDRFSGSGSGDFTLKISRVEAEVGVYYCMQALCP-TF					Section 3
	(103)	103 111					
CUR2-1.11.1 LC	(103)	GGGPKVEIK					
A19	(101)	-----					
Consensus	(103)	-----					

FIGURE 25Figure 25A

	(1)	10	20	30	40	50	Section 1
CR2-1.17.1 HC VH3-33	(1) QVQLVEGGGVVQPCRLRSLCAAAGFTFSYYGMHHVRQAPGKGLEWVA VI						
Consensus	(1) QVQLVEGGGVVQPGKSLRLSCAAAGFTFSYYGMHHVRQAPGKGLEWVA VI						
	(52) 52	60	70	80	90	102	Section 2
CR2-1.17.1_HC VH3-33	(52) WYDGSNKKYYADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYCARQGY						
Consensus	(52) WYDGSNKKYYADSVKGRPTISRDNSKNTLYLQMNSLRAEDTAVYCAR---						
	(103) 103	110	120				Section 3
CR2-1.17.1_HC VH3-33	(103) RYAGYYDDYGMWDVGQGTTVTVS						
Consensus	(103) -----						

Figure 25B

	(1)	10	20	30	40	50	Section 1
CR2-1.17.1_LC A30	(1) DICMTQSPSSLSASVGDRAVTITCRASQQIRNDLGWYQQRPGKAPKRLLIYAA S						
Consensus	(1) DICMTQSPSSLSASVGDRAVTITCRASQQIRNDLGWYQQRPGKAPKRLLIYAA S						
	(53) 53	60	70	80	90	104	Section 2
CR2-1.17.1_LC A30	(53) SLQSGVPSSRFSSGSGGTEFTLTISLQPEDPATYYCLQHNSYP-----						
Consensus	(53) SLQSGVPSSRFSSGSGBTEFTLTISLQPEDPATYYCLQHNSYP						
	(105) 105	1067					Section 3
CR2-1.17.1_LC	(105) EIK						
A30	(96) ---						
Consensus	(105)						



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*Corvalan et al.*  
Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 26

Figure 26A

	1	10	20	30	40	52	Section 1
CR2-1.1B_HC	(1) QVQLVQSGAEVKKPGASVCKASGYTFTSYDINNVRQATGQGLEMGWMN						
VH1-8	(1) QVQLVQSGAEVKKPGASVCKASGYTFTSYDINNVRQATGQGLEMGWMN						
Consensus	(1) QVQLVQSGAEVKKPGASVCKASGYTFTSYDINNVRQATGQGLEMGWMN						Section 2
	(53) S3	60	70	80	90	104	
CR2-1.1B_HC	(53) PNSGNTGVAQKPFQGRVTMTRNTSISSTAYMELSSLSEDATAVYYCAEGIAVA						
VH1-8	(53) PNSGNTGVAQKPFQGRVTMTRNTSISSTAYMELSSLSEDATAVYYCAEGIAVA						
Consensus	(53) PNSGNTGVAQKPFQGRVTMTRNTSISSTAYMELSSLSEDATAVYYCAEGIAVA						Section 3
	(105) 105	110	115	120	126		
CR2-1.1B_HC	(105) GTYYYYYGGMDVWGGGTTTVSS						
VH1-8	(99) -----						
Consensus	(105)						

Figure 26B

	1	10	20	30	40	53	Section 1
CR2-1.1B_LC	(1) DIQONTSPSSLSASVGDRVTITCRASQGIRNRDLGWYQOKPGKAPRKLIVYASS						
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNRDLGWYQOKPGKAPRKLIVYASS						
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNRDLGWYQOKPGKAPRKLIVYASS						Section 2
	(54) 54	60	70	80	90	106	
CR2-1.1B_LC	(54) LQSGVPSRFSGSGSGTEFTLTISLQPEDPATYCLQHNSYPFTFGPGTKVDI						
A30	(54) LQSGVPSRFSGSGSGTEFTLTISLQPEDPATYCLQHNSYP-----						
Consensus	(54) LQSGVPSRFSGSGSGTEFTLTISLQPEDPATYCLQHNSYP						Section 3
	(107) K						
CR2-1.1B_LC	(107) K						
A30	(96) -						
Consensus	(107)						

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Corvalan et al.

Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 27Figure 27A

	(1)	10	20	30	40	52	Section 1
Cur2-1.19.1 lc	(1) QVQLVQSGAEAVKPGASVKV9CKASGYEPRSYDINWVRQARGQGLEWMGMM						
A30	(1) QVQLVQSGAEAVKPGASVKV9CKASGYEPTSYDINWVRQATGGLEWMGMM						
Consensus	(1) QVQLVQSGAEAVKPGASVKV9CKASGYPTSYDINWVRQATGGLEWMGMM						
							Section 2
	(53) 53	60	70	80	90	104	
Cur2-1.19.1_lc	(53) PNSGNTGTYAQNFOGRVTRNTSI8TAXMELSSRLSEDTAVYYCARVMITF						
A30	(53) PNSGNTGTYAQNFOGRVTRNTSI8TAXMELSSRLSEDTAVYYCAR-----						
Consensus	(53) PNSGNTGTYAQNFOGRVTRNTSI8TAXMELSSRLSEDTAVYYCAR-----						
							Section 3
	(105) 105	110	120	126			
Cur2-1.19.1_lc	(105) GGVIVHYGMDVWQGQTTTVSS						
A30	(99) -----						
Consensus	(105)						

Figure 27B

	(1)	10	20	30	40	52	Section 1
Cur2-1.19.1 lc	(1) DIQMTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLLIXAA						
A30	(1) DIQMTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLLIXAA						
Consensus	(1) DIQMTQSPSSLSASVGDRTITCRASQGIRNDLGWYQQKPGKAPKRLLIXAA						
							Section 2
	(53) 53	60	70	80	90	104	
Cur2-1.19.1_lc	(53) SLSQSGVPSRFSRGSGSSTFTLTISSLOPEDFATYYCLOHNSDPCSFQGQTEL						
A30	(53) SLSQSGVPSRFSRGSGSSTFTLTISSLOPEDFATYYCLOHNSYF-----						
Consensus	(53) SLSQSGVPSRFSRGSGSSTFTLTISSLOPEDFATYYCLOHNS F						
							Section 3
	(105) 1057						
Cur2-1.19.1_lc	(105) EIR						
A30	(96) ---						
Consensus	(105)						



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Corvalan et al.  
Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

### FIGURE 28

Figure 28A

	(1)	10	20	30	40	51	Section 1
Cur2-1.231_HC	(1) EVQLVQSGAEVKRKGESLKIICG						
VH5-51	(1) EVQLVQSGAEVKRKGESLKIICG						
Consensus	(1) EVQLVQSGAEVKRKGESLKIICG						
	(2)	52	60	70	80	90	102
Cur2-1.231_HC	(2) YPGDSDTRYSPSPQQVTISADKSISTAYLQWSSSLKA						
VH5-51	(2) YPGDSDTRYSPSPQQVTISADKSISTAYLQWSSSLKA						
Consensus	(2) YPGDSDTRYSPSPQQVTISADKSISTAYLQWSSSLKA						
	(103)	103	110	126			
Cur2-1.231_HC	(103) YYVSGSYVNVFDYWGQGTLVTVSS						
VH5-51	(69) -----						
Consensus	(103)						

Figure 28B

	(1)	10	20	30	40	51	Section 1
Cur2-1.231_LC	(1) DIQMTOQSESSLASAVGDRVTITCRASQGIRNDLGWYQ						
A30	(1) DIQMTOQSESSLASAVGDRVTITCRASQGIRNDLGWYQ						
Consensus	(1) DIQMTOQSESSLASAVGDRVTITCRASQGIRNDLGWYQ						
	(2)	52	60	70	80	90	102
Cur2-1.231_LC	(2) S8LQRGVVBRFBQGSGTEFTLTIS8LQPSDFATYVCLQHNSYBWTFGQT						
A30	(2) S8LQRGVVBRFBQGSGTEFTLTIS8LQPSDFATYVCLQHNSYB-----						
Consensus	(2) S8LQ GVE SRF SGSGSGTEFTLTIS8LQPSDFATYVCLQHNSYB						
	(103)	103	107				
Cur2-1.231_LC	(103) KVEIK						
A30	(69) -----						
Consensus	(103)						



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 Corvalan et al.  
 Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 29

Figure 29A

	(1)	10	20	30	40	50	Section 1
CR2-1.24.1_HC	(1)	QVOLVERGGGVQPGRSRLSCAAAGP	FSSYGMHNVRQAPGKGLEWVA	D			
VH3-33	(1)	QVOLVERGGGVQOPGRSLRLSCAAAGP	FSSYGMHNVRQAPGKGLEWVA	V			
Consensus	(1)	QVOLVERGGGVQPGRSRLSCAAAGP	FSSYGMHNVRQAPGKGLEWVA	I			
	(52)	52	60	70	80	90	102
CR2-1.24.1_HC	(52)	WYDGSBNKYYADSVFGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARQD	G				
VH3-33	(52)	WYDGSBNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	---				
Consensus	(52)	WYDGSBNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	---				
	(103)	103	110	125			
CR2-1.24.1_HC	(103)	SYGYYYYDYGMDWGQGTTVTVSS					
VH3-33	(99)	-----					
Consensus	(103)	-----					

Figure 29B

	(1)	10	20	30	40	50	Section 1
CR2-1.24.1_LC	(1)	DIQMTQSPSPLASAVGDEVTITCRASOGIRNDLGWYQOKPGKAPKRLLIYAA	S				
A30	(1)	DIQMTQSPSPLASAVGDRVTITCRASOGIRNDLGWYQOKPGKAPKRLLIYAA	S				
Consensus	(1)	DIQMTQSPSPLASAVGDRVTITCRASOGIRNDLGWYQOKPGKAPKRLLIYAA	S				
	(53)	53	60	70	80	90	104
CR2-1.24.1_LC	(53)	SIQSGVPSRFSQSGGGTETFTLTISLOPEDFATYYCLQHNSYVNTFGQGDKV					
A30	(53)	SIQSGVPSRFSQSGGGTETFTLTISLOPEDFATYYCLQHNSYV	-----				
Consensus	(53)	SIQSGVPSRFSQSGGGTETFTLTISLOPEDFATYYCLQHNSYV	-----				
	(105)	105	106	107			
CR2-1.24.1_LC	(105)	EIK					
A30	(96)	---					
Consensus	(105)	---					



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Corvalan et al.  
Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

**FIGURE 30**

**Figure 30A**

	(1) 1	10	20	30	40	51	Section 1
VH5-51	(1) EVQLVQSGAEIVKPGESNLKISCKGSGYFTSYWIGWVRQMPGKLEWMGII						
CR2-1.25.1_HC	(1) EVQLVQSGAEIVKPGESNLKISCKGSGYFTSYWIGWVRQMPGKLEWMGII						
Consensus	(1) EVQLVQSGAEIVKPGESNLKISCKGSGY FT SYWIGWVRQMPGKLEWMGII						
	(2) 52	60	70	80	90	102	Section 2
VH5-51	(2) YFGDSDTRYSPFQSGQVTISADKSISTAYLQWSSLKA SDTAMYXCAR ---						
CR2-1.25.1_HC	(2) YFGDSDTRYSPFQSGQVTISADKSISTAYLQWSSLKA SDTAMYXCAR HG SY						
Consensus	(2) YFGDSDTRYSPFQSGQVTISADKSISTAYLQWSSLKA SDTAMYXCAR						
	(10) 103	110	126				Section 3
VH5-51	(10) -----						
CR2-1.25.1_HC	(10) YYGSETYYNVFDYWGQGTLTVSS						
Consensus	(10)						

**Figure 30B**

	(1) 1	10	20	30	40	52	Section 1
A30	(1) DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQTGGKAPKRLLIYAA						
CR2-1.25.1_LC	(1) DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQTGGKAPKRLLIYAA						
Consensus	(1) DIQMTQSPSSLSASVGDRVITCRASQGIRNDLGWYQQTGGKAPKRLLIYAA						
	(53) 53	60	70	80	90	104	Section 2
A30	(53) SLOSGVFSRFSGS6SGTEFTLTISLOPEDFATYYCLOHNSYPE -----						
CR2-1.25.1_LC	(53) SLOSGVFSRFSGS6SGTEFTLTISLOPEDFATYYCLOHNSYPETFQGQTKV						
Consensus	(53) SLOSGVFSRFSGS6SGTEFTLTISLOPEDFATYYCLOHNSYPE						
	(105) 1097						Section 3
A30	(105) -----						
CR2-1.25.1_LC	(105) EIK						
Consensus	(105)						



**FIGURE 31**

**Figure 31A**

	1	10	20	30	40	50	Section 1
VH5-51	(1)						
CR2-1.29_HC	(1)	EVOVLVOSGAEVKRPGESLKLISCKRGCGVSPFTSYWIGWVRQMPGKGLENMGIIY					
Consensus	(1)	EVOVLVOSGAEVKRPGESLKLISCKRGCGVSPFTSYWIGWVRQMPGKGLENMGIIY					
							Section 2
VH5-51	(53)	53	60	70	80	90	104
CR2-1.29_HC	(53)	PGDSDTRYSPFGQQ	TISADKSITAYLQWSSLKA	D	TANYYCAR	-----	
Consensus	(53)	PGDSDTRYSPFGQQ	TISADKSITAYLQWSSLKA	D	TANYYCAR	HUVDVG	
							Section 3
VH5-51	(105)	105	110	129			
CR2-1.29_HC	(105)	TIGGYYYYYYHGM	DVWGQGTTVT	VSS			
Consensus	(105)						

**Figure 31B**

	1	10	20	30	40	50	Section 1
A19	(1)						
CR2-1.29_LC	(1)	DIVMTQSPLSLPVTPGEPA	SICR3SQSLLHSNGYNLYDWYLQKPGCSPOLLI				
Consensus	(1)	DIVMTQSPLSLPVTPGEPA	SICR3SQSLLHSNGYNLYDWYLQKPGCSPOLLI				
							Section 2
A19	(54)	54	60	70	80	90	106
CR2-1.29_LC	(54)	YLGSRASGVDPFGSGS	G6GTDFTLKISRVEA	DVGVYVYCMQALQ	-----		
Consensus	(54)	YLGSRASGVDPFGSGS	G6GTDFTLKISRVEA	DVGVYVYCMQALQ	LMCSFGQ		
							Section 3
A19	(107)	107	113				
CR2-1.29_LC	(107)	GTKLEIK					
Consensus	(107)						



10004-1960 . 081302  
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*Corvalan et al.*  
 Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

**FIGURE 32**

**Figure 32A**

	(1)	1	10	20	30	40	50	Section 1
VH1-18	(1)	QVQLVQSGAEVKKPGASVVKVKCKASGYTFTSAYGIGISWVRQAPGQGLEWMGWIS						
CR2-1.33_HC	(1)	QVQLVQSGAEVKKPGASVVKVKCKASGYTFTSAYGIGISWVRQAPGQGLEWMGWIS						
Consensus	(1)	QVQLVQSGAEVKKPGASVVKVKCKASGYTFTSAYGIGISWVRQAPGQGLEWMGWIS						
								Section 2
VH1-18	(63)	AYNGNTNYAACQLQGRVTMSTDTSSTAYMELRSLRSDDTAVYYCAR-----	53	60	70	80	90	104
CR2-1.33_HC	(63)	AYNGNTNYAACQLQGRVTMSTDTSSTAYMELRSLRSDDTAVYYCAR-----						
Consensus	(63)	AYNGNTNYAACQLQGRVTMSTDTSSTAYMELRSLRSDDTAVYYCAR-----						
								Section 3
VH1-18	(105)	SDYLYYYYYGLDVWSQQGTTVTVSS	105	110	120	127		
CR2-1.33_HC	(105)	SDYLYYYYYGLDVWSQQGTTVTVSS						
Consensus	(105)	SDYLYYYYYGLDVWSQQGTTVTVSS						

**Figure 32B**

	(1)	1	10	20	30	40	50	Section 1
A20	(1)	DIONQDSESSISASVGDRVLTICRAASQGIGSNYLANYQOKPGKVKPLLLYAAST						
CR2-1.33_LC	(1)	DIONQDSESSISASVGDRVLTICRAASQGIGSNYLANYQOKPGKVKPLLLYAAST						
Consensus	(1)	DIONQDSESSISASVGDRVLTICRAASQGIGSNYLANYQOKPGKVKPLLLYAAST						
								Section 2
A20	(64)	LQSGVPSPRFSGSGSGGTDPFTLTISSLOPELVAATYYCQKYNAP-----	54	60	70	80	90	106
CR2-1.33_LC	(64)	LQSGVPSPRFSGSGSGGTDPFTLTISSLOPELVAATYYCQKYNAP-----						
Consensus	(64)	LQSGVPSPRFSGSGSGGTDPFTLTISSLOPELVAATYYCQKYNAP-----						
								Section 3
A20	(66)	-	107	107				
CR2-1.33_LC	(107)	K						
Consensus	(107)							

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Corvalan et al.  
Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

**FIGURE 33**

**Figure 33A**

	(1)	10	20	30	40	51	
VH-33	(1)	QVQLVERGGGVVQPGADSLRLSCAASGCFESSYGMHMVRQAPGKGLEWVAII					
CR2-1.3B.1_HC	(1)	QVQLVERGGGVVQPGRSI RLSCAASGCFESSYGMHMVRQAPGKGLEWVAII					
Consensus	(1)	QVCLVERGGGVVQPGRSI RLSCAASGCFESSYGMHMVRQAPGKGLEWVAII					
						Section 1	
	(52)	52	60	70	80	90	
VH-33	(52)	WYDGSNRYVADSVKGRFTI RDNSKNTLYLQMNSLRAEDTAVYYCAR---					Section 2
CR2-1.3B.1_HC	(52)	WYDGNDRKVYADSVKGRFTI RDNSKNTLYLQMNSLRAEDTAVYYCARGYYY					
Consensus	(52)	WYDG KYYADSVKGRFTI RDNSKNTLYLQMNSLRAEDTAVYYCAR					
	(103)	103	110		127		Section 3
VH-33	(103)	DS SDYLYYYYYGMDVWGQGT TVTVSS					
CR2-1.3B.1_HC	(103)	-----					
Consensus	(103)	-----					

**Figure 33B**

	(1)	10	20	30	40	52	
A20	(1)	DIGMTQSPSSLASAVGDRVITCRASOGISNYLAWYQQKPGKVPKLLIYAA3					
CR2-1.3B.1_LC	(1)	LIGMTQSPSSLASAVGDRVITCRASOGISNYLAWYQQKEGKVPENLLIYAA3					
Consensus	(1)	DIGMTQSPSSLASAVGDRVITCRASOGISNYLAWYQQKPGKVP LLIYAA3					
	(53)	53	60	70	80	90	Section 2
A20	(53)	TIQSGVPSPRGSGSGTDFLTIS SLOPEDVATYYCQKNSAP-----					
CR2-1.3B.1_LC	(53)	TIQSGVPSPRGSGSGTDFLTIS SLOPEDVAAYYCQRCNSAFMTPFGQGTTV					
Consensus	(53)	TIQSGVPSPRGSGSGTDFLTIS SLOPEDVA YYCOK NSAP					
	(106)	106	107				Section 3
A20	(106)	---					
CR2-1.3B.1_LC	(106)	EIK					
Consensus	(106)	-----					

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Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 34

Figure 34A

	(1)	10	20	30	40	51	Section 1
VH5-51	(1) BVQIYQBSAAVKKRPGESLKIISCKGSGYSPFTSYWIGMWVRQMPDONGELBWMGII						
CR2-1.39.1_HC	(1) EVOLVQGSTEVKKRPGESELKISCTGGSYRFTSYWIGMWVRQMPDGVGLEWMGII						
Consensus	(1) EVOLVQSGEVKRPGESELKISCKGSGY FTSYWIGMWVRQMPDGVGLEWMGII						
	(52)	60	70	80	90	102	Section 2
VH5-51	(52) YPGDSDTRYSPSFQGGVTLISADKSISTAYLQWNSSLKASDPTAMYCAR---						
CR2-1.39.1_HC	(52) YPGDSDTRYSPSFQGGVTLISADKSISTAYLQWNSSLKASDPTAMYCARAHGSY						
Consensus	(52) YPGDSDTRYSPSFQGGVTLISADKSISTAYLQWNSSLKASDPTAMYCAR						Section 3
	(103)	103	110	126			
VH5-51	(103) -----	(99)	-----				
CR2-1.39.1_HC	(103) YYN8GSYYNNPFDYWGQGTIVTVSS						
Consensus	(103)						

Figure 34B

	(1)	10	20	30	40	52	Section 1
A30	(1) DIQMTQSPSLSASAVGDRVITCRASQGIRNDLGWYQOKPDKAFKR2IYAA8						
CR2-1.39.1_LC	(1) DIQMTQSPSLSASAVGDRVITCRASQGIRNDLGWYQOKPDKAFKR2IYAA8						
Consensus	(1) DIQMTQSPSLSASAVGDRVITCRASQGIRNDLGWYQOKPDKAFKR2IYAA8						
	(53)	60	70	80	90	104	Section 2
A30	(53) SIQSGVPSPRFSGSGSGTETFTLTSISSLQPEDPATYYCLQHN8YP-----						
CR2-1.39.1_LC	(53) SIQSGVPSPRFSGSGSGTETFTLTSISSLQPEDPATYYCLQHN8YPWTFGQGRKV						
Consensus	(53) SIQSGVPSPRFSGSGSGTETFTLTSISSLQPEDPATYYCLQHN8YP						
	(105)	105	106	107			
A30	(105) ---	(96)	---				
CR2-1.39.1_LC	(105) EIK						
Consensus	(105)						

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Appl. No.: 10/041,860 Atty Docket: ABGENIX 051A

FIGURE 35

Figure 35A

	(1)	1	10	20	30	40	50	Section 1
VH1-8	(1)	QVQLVQSGAEVKKPGASA CR2-1.45_HC	QVQLVQSGAEVKKPGASA Consensus	VKVKSCASGYTFTSYDINWVRQATGQGLEWMGWMM				
	(1)	QVQLVQSGAEVKKPGASA CR2-1.45_HC	QVQLVQSGAEVKKPGASA Consensus	VKVKSCASGYTFTSYDINWVRQATGQGLEWMGWMM				Section 2
	(53)	53	60	70	80	90		104
VH1-8	(53)	PNSGNNTGYAQQKFQGRVUTMNTSISTAYMELSSLRSED CR2-1.45_HC	PNSGNNTGYAQQKFQGRVUTMNTSISTAYMELSSLRSED Consensus	TAVYYCARGSGGSY				
	(53)	PNSGNNTGYAQQKFQGRVUTMNTSISTAYMELSSLRSED CR2-1.45_HC	PNSGNNTGYAQQKFQGRVUTMNTSISTAYMELSSLRSED Consensus	TAVYYCAR				Section 3
	(105)	105	110	125				
VH1-8	(99)	-----						
CR2-1.45_HC	(105)	GYDYYYYGMDVNGQGTTVTVS						
Consensus	(105)							

Figure 35B

	(1)	1	10	20	30	40	50	Section 1
A20	(1)	DIQMTOQPSSLSASVGDRVTITCRASQG	S NYLAWYQOKPGKUPKLILYYA	AST				
CR2-1.45_LC	(1)	DIQMTOQPSSLSASVGDRVTINCRASQG	S ND LAWYQOKPGKUPKLILYYA	AST				
Consensus	(1)	DIQMTOQPSSLSASVGDRVTI	CRASQG ISN	LAWYQOKPGKUPKLILYYA	AST			Section 2
	(54)	54	60	70	80	90		106
A20	(54)	LGSGVPSSRFSGSGSGTDFITLTISLDQPED	VATYYCQKYNSAP	-----				
CR2-1.45_LC	(54)	LGOLVESRESSSGSGSGDPELTLLISLDQ	ELVATYYCQKYNSAP	PTPGPGTKVDI				
Consensus	(54)	LQ	GVPSSRFSGSGSGTDFITLTISLDQPED	VATYYCQKYNSAP				Section 3
	(107)	107						
A20	(56)	-						
CR2-1.45_LC	(107)	K						
Consensus	(107)							

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Corvalan et al.  
Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 36

Figure 36A

	(1)	10	20	30	40	51	Section 1
VH1-8	(1) QVQIVQSGAEVKKPGASVVKVSCKASGYFTSYDINVRQATGQGLEWMGMW						
CR2-1.46.1_HC	(1) QVQIVQSGAEVKKPGASVVKVSCKASGYFTSYDINVRQATGQGLEWMGMW						
Consensus	(1) QVQIVQSGAEVKKPGASVVKVSCKASGYFTSYDINVRQATGQGLEWMGMW						
	(52)	52	60	70	80	90	102
VH1-8	(52) NPNNGNGSYAQKFQGRVUTMTRNTSISTAYNELLSSRLSEDTAVYYCAR---						
CR2-1.46.1_HC	(52) NPNNGNGSYAQKFQGRVUTMTRNTSISTAYNELLSSRLSEDTAVYYCARVV						
Consensus	(52) NPN GNTGYAQQKFQGRVUTMTRNTSISTAYNELLSSRLSEDTAVYYCAR						
	(103)	103	110	126			
VH1-8	(103) VVTATDYYYYGMDVWGQGTTTVSS						
CR2-1.46.1_HC	(103) VVTATDYYYYGMDVWGQGTTTVSS						
Consensus	(103)						

Figure 36B

	(1)	10	20	30	40	52	Section 1
A30	(1) DIQMTQSPSLSASVGDRVTISRASQGIRNDLGWYQQKPGKAQKRLIIPAAAS						
CR2-1.46.1_LC	(1) DIQMTQSPSLSASVGDRVTISRASQGIRNDLGWYQQKPGKAQKRLIIPAAAS						
Consensus	(1) DIQMTQSPSLSASVGDRVTISRASQGIRNDLGWYQQKPGKAQKRLIIPAAAS						
	(53)	53	60	70	80	90	104
A30	(53) SWQSGVPSRSGSGSGTBTTLTISLLOPEDFATYYCLQHN3YP-----						
CR2-1.46.1_LC	(53) SWQSGVPSRSGSGSGTBTTLTISLLOPEDFATYYCLQHSGYPPTFQGQTKV						
Consensus	(53) SL SGVP SRSGSGSGTEFTLTISLLOPEDFATYYCLQH YP						
	(105)	105	107				
A30	(105) ---						
CR2-1.46.1_LC	(105) EIK						
Consensus	(105)						

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Corvalan et al.

Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

10041960 .081302

**FIGURE 37**

**Figure 37A**

	(1)	10	20	30	40	51	Section 1
CR2-1.4B.1 HC	(1) QVQLVQSGAENVKPGASVVKVSCAKASGYTFPSVGSWVRQAPGQGLEWMGMIZ						
VH1-18	(1) QVQLVQSGAENVKPGASVVKVSCAKASGYTFPSVGSWVRQAPGQGLEWMGMIZ						
Consensus	(1) QVQLVQSGAENVKPGASVVKVSCAKASGYTFPSVGSWVRQAPGQGLEWMGMIZ						
	(52)	60	70	80	90	102	Section 2
CR2-1.4B.1 HC	(52) SAYNGNTNHYAQKLQGRGRTMTDSTSTAYMELRSRSDDTAVYYCARVVEY						
VH1-18	(52) SAYNGNTNHYAQKLQGRGRTMTDSTSTAYMELRSRSDDTAVYYCAR---						
Consensus	(52) SAYNGNTNHYAQKLQGRGRTMTDSTSTAYMELRSRSDDTAVYYCAR-						
	(103)	110	125				Section 3
CR2-1.4B.1 HC	(103) YYDGGGGYYYYPDYWGQQTIVTVSS						
VH1-18	(99) -----						
Consensus	(103)						

**Figure 37B**

	(1)	10	20	30	40	52	Section 1
CR2-1.4B.1 LC	(1) DIQMTOBSPSSVSASVGDRVTITCRASQGIGSSMWLAWYQOKPGKAPKLLIYAA						
L5	(1) DSQMTQSPSPSSVSASVGDRVTITCRASQGIGSSMWLAWYQOKPGKAPKLLIYAA						
Consensus	(1) DIQMTOBSPSSVSASVGDRVTITCRASQGIGSSMWLAWYQOKPGKAPKLLIYAA						
	(53)	60	70	80	90	104	Section 2
CR2-1.4B.1 LC	(53) ILQSGGVFSPRFSSGSGSGTDFTLTISLQPEDPFAVYCOOANSFPRTFGQQGTV						
L5	(53) SLSQSGGVFSPRFSSGSGSGTDFTLTISLQPEDPFAVYCOOANSFP-----						
Consensus	(53) LQSGGVFSPRFSSGSGSGTDFTLTISLQPEDFASYCQQANSFP						
	(105)	1087					Section 3
CR2-1.4B.1 LC	(105) EIK						
L5	(96) ---						
Consensus	(105)						

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Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 38

Figure 38A

	(1)	10	20	30	40	51	Section 1
CR2-1.49.1 HC	(1) QVQLVQSGAEAVKPGASVKVSKCAGSYFTSYDINWVRQATGOGLEWMGWM						
VH1-8	(1) QVQLVQSGAEAVKPGASVKVSKCAGSYFTSYDINWVRQATGOGLEWMGWM						
Consensus	(1) QVQLVQSGAEAVKPGASVKVSKCAGSYFTSYDINWVRQATGOGLEWMGWM						
							Section 2
CR2-1.49.1 HC	(52) NPNSGSDTGYAQKFGQRVUTMTRNTSISTAYMELSSRLSEDATAVYFCAR	52	60	70	80	90	102
VH1-8	(52) NPNSGSDTGYAQKFGQRVUTMTRNTSISTAYMELSSRLSEDATAVYFCAR						
Consensus	(52) NPNSGSDTGYAQKFGQRVUTMTRNTSISTAYMELSSRLSEDATAVYFCAR						
							Section 3
CR2-1.49.1 HC	(103) VATSYYFYGMDVWGQGTTVTVS	103	110	117			
VH1-8	(99) -----						
Consensus (103)							

Figure 38B

	(1)	10	20	30	40	52	Section 1
CR2-1.49.1 LC	(1) DIVMTQSPLSLFVTPGEPASISCRSSQ3LLHSNGNYNLDWYLKPGQSPOLL						
A19	(1) DIVMTQSPLSLFVTPGEPASISCRSSQ3LLHSNGNYNLDWYLKPGQSPOLL						
Consensus	(1) DIVMTQSPLSLFVTPGEPASISCRSSQ3LLHSNGNYNLDWYLKPGQSPOLL						
							Section 2
CR2-1.49.1 LC	(53) IYLGSSPASGVDPDRFSGSGSGTDLXKISRVEADVGVVYCMOTLQITFFGQ	53	60	70	80	90	104
A19	(53) IYLGSSPASGVDPDRFSGSGSGTDLXKISRVEADVGVVYCMOTLQITFFGQ						
Consensus	(53) IYLGSSPASGVDPDRFSGSGSGTDLXKISRVEADVGVVYCMOTLQITFFGQ						
							Section 3
CR2-1.49.1 LC	(105) GTRLEIK	105	111				
A19 (101)	(105) GTRLEIK						
Consensus (105)							

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 Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

**FIGURE 39**

**Figure 39A**

	1	10	20	30	40	50	Section 1
CR2-1.51.1 HC	(1) 1						
V45-51	(1) EVOLVQSGAEVKRPGEGLKIKCKGSCGSCGYSPTSYWIGMVRQMPGKGLENWGII						
Consensus	(1) EVOLVQSGAEVKRPGEGLKIKCKGSCGSCGYSPTSYWIGMVRQMPGKGLENWGII						
							Section 2
CR2-1.51.1 HC	(52) 52	60	70	80	90	102	
V45-51	(52) YPGD8DA YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCARHYDY						
Consensus	(52) YPGD8DA YSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR---						
							Section 3
CR2-1.51.1 HC	(103) 103	110	120				
V45-51	(103) VWRNRYTYGWFDPWGGQTLYTVSS						
Consensus	(103)						

**Figure 39B**

	1	10	20	30	40	50	Section 1
CR2-1.51.1 LC	(1) 1						
A27	(1) EIVLTQSPGTLSLSPGERALSCRASQSVSSSYLAWYQQKPGQAERLLIYGA						
Consensus	(1) EIVLTQSPGTLSLSPGERALSCRASQSVSSSYLAWYQQKPGQAERLLIYGA						
							Section 2
CR2-1.51.1 LC	(53) 53	60	70	80	90	104	
A27	(53) SRRATGIPDRFSGSGGSGGTDFLTISRLPEPDAVYYCQQYGSSLFTPGPGTK						
Consensus	(53) SRRATGIPDRFSGSGGSGGTDFLTISRLPEPDAVYYCQQYGSSP-----						
							Section 3
CR2-1.51.1 LC	(105) 105	108					
A27	(105) VDIR						
Consensus	(105)						

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10041860 .081302

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*Corvalan et al.*  
 Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

### FIGURE 40

Figure 40A

	(1)	10	20	30	40	50	52	Section 1
CuI2-6.4.1 hc	(1) QVQLVQSGAEVVKREGASVTSKASGVTPTSYDINWWVRQATGGGLEVMGDN							
VH1-8	(1) QVQLVQSGAEVVKREGASVTSKASGVTPTSYDINWWVRQATGGGLEVMGDN							
Consensus	(1) QVQLVQSGAEVVKREGASVTSKASGVTPTSYDINWWVRQATGGGLEVMGDN							
	(53) 53	60	70	80	90			Section 2
CuI2-6.4.1 hc	(53) PNSGNTWVACRFPQGRFTMTRDSESTAYMELSSRSRSDTA-----							
VH1-8	(53) PNSGNTWVACRFPQGRFTMTRDSESTAYMELSSRSRSDTA-----							
Consensus	(53) PNSGNTWVACRFPQGRFTMTRDSESTAYMELSSRSRSDTA-----							
	(105) 105	110	125					Section 3
CuI2-6.4.1 hc	(105) NYDYYIGMDVWGCGTTVTIVSS							
VH1-8	(99) -----							
Consensus	(105)							

Figure 40B

	(1)	10	20	30	40	50	52	Section 1
CuI2-6.4.1 Lc	(1) EIVLTQSPGTLISLSPGERATLSKCRASQS VSSSYLAWYQQKPGQAPRLIYA							
A27	(1) EIVLTQSPGTLISLSPGERATLSKCRASQS VSSSYLAWYQQKPGQAPRLIYA							
Consensus	(1) EIVLTQSPGTLISLSPGERATLSKCRASQS VSSSYLAWYQQKPGQAPRLIYA							
	(53) 53	60	70	80	90			Section 2
CuI2-6.4.1 Lc	(53) S5RATGIPDRFSSGSGSSTDFTLTISRLLEPEDFAVYYCQGYGSSCSCFGQGDK							
A27	(53) S5RATGIPDRFSSGSGSSTDFTLTISRLLEPEDFAVYYCQGYGSSCSCFGQGDK							
Consensus	(53) S5RATGIPDRFSSGSGSSTDFTLTISRLLEPEDFAVYYCQGYGSSP							
	(105) 105	109	109					Section 3
CuI2-6.4.1 Lc	(105) LEIK							
A27	(97) -----							
Consensus	(105)							

Clone #	VH L	#DR	VH end	# N's	N Sequence	DH	Size or D	D Sequence	# N's	JK	# del	JH Segment	
1.19. 1	DP-15/1- 8	-1	CAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TGATGATACCTT GGCGGATTATCCT (SEQ ID NO:93)	2	GC	JH6	-12	ACTACG (SEQ ID NO:94)
1.19. 2	DP-15/1- 8	-1	CAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TGATGATACCTT GGCGGATTATCCT (SEQ ID NO:93)	2	GC	JH6	-12	ACTACG (SEQ ID NO:94)
1.19. 3	DP-15/1- 8	-1	CAGAG (SEQ ID NO:92)	3	ACG	D3-16	28	TGATGATACCTT GGCGGATTATCCT (SEQ ID NO:93)	2	GC	JH6	-12	ACTACG (SEQ ID NO:94)
6.4.1	DP-15/1- 0		GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGATGATACCTA (SEQ ID NO:96)	2	TA	JH6	0	ATRACTAC (SEQ ID NO:97)
6.4.2	DP-15/1- 0		GAGAGG (SEQ ID NO:95)	3	CTT	D5-18	12	TGATGATACCTA (SEQ ID NO:96)	2	TA	JH6	0	ATRACTAC (SEQ ID NO:97)
6.4.3	DP-15/1- 0		GAGAG (SEQ ID NO:95)	3	CTT	D5-18	12	TGATGATACCTA (SEQ ID NO:96)	2	TA	JH6	0	ATRACTAC (SEQ ID NO:97)

Figure 41A

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 Appl. No.: 10/041,860. Atty Doc#: ABGEN051A  
 Corradini et al.



1.19. 3	A30	-3	TTGACC	6	GTGCGA	JTC2	-7	TTTGGG (SEQ ID NO:198)
6.4.1	A27/A27A	-3	CTGACCC	6	GTGCGA	JTC2	-7	TTTGGG (SEQ ID NO:100)
6.4.2	A27/A27A	-3	ATG	6	GTGCGA	JTC2	-7	TTTGGG (SEQ ID NO:103)
6.4.3	A27/A27A	-3	CTGACCC	6	GTGCGA	JTC2	-7	TTTGGG (SEQ ID NO:103)
			ATG	6	GTGCGA	JTC2	-7	TTTGGG (SEQ ID NO:103)
			ATG	6	GTGCGA	JTC2	-7	TTTGGG (SEQ ID NO:103)

Figure 41B

ANTIBODIES DIRECTED TO PGF2 AND USES THEREOF  
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Clone #	VH	# Del.	Vk end	# Ns	N sequence	DH size of D	D sequence	# Ns	JK sequence	JK del. segment	
1.6.1	DP-77/3-21	0	GAGAA (SEQ ID NO:104)	0		D3-16	22	TATATGATTC GTTGGGGA (SEQ ID NO:105)	14	ATTATGCC TCCTT (SEQ ID NO:106)	-1
1.6.1	DP-77/3-21	0	GAGAA (SEQ ID NO:104)	0		D3-16	22	TATATGATTC GTTGGGGA (SEQ ID NO:105)	14	ATTATGCC TCCTT (SEQ ID NO:106)	-1
1.6.1	DP-77/3-21	0	GAGAA (SEQ ID NO:104)	0		D3-16	22	TATATGATTC GTTGGGGA (SEQ ID NO:105)	14	ATTATGCC TCCTT (SEQ ID NO:106)	-1
1.11.1	DP-42/3-53	-5	AAGAA (SEQ ID NO:109)	3	GGA	D4-17	10	ACGCGACTA GTTGGGGA (SEQ ID NO:105)	5	CGAAAT TCCTT (SEQ ID NO:106)	-2
1.11.2	DP-42/3-53	-5	AAGAA (SEQ ID NO:109)	3	GGA	D4-17	10	ACGCGACTA GTTGGGGA (SEQ ID NO:109)	5	CGAAAT TCCTT (SEQ ID NO:110)	-2
1.23.1	DP-73/5-51	0	GAGACCA	16	TGTATGATTC	D3-10	19	TTCGGGAGTA ATGT (SEQ ID NO:112)	2	GT	JKAB
1.23.2	DP-73/5-51	0	GAGACCA	16	TGTATGATTC	D3-10	19	TTCGGGAGTA ATGT (SEQ ID NO:112)	2	GT	JKAB

Figure 42A

APPL. NO.: 10/041,860 Atty/Deckt: ABGENEX/OSIA  
 Cognaclo et al. ATTBODIES DIRECTED TO PCDP AND USES THEREOF

10041360.D081302



**Figure 42B**

ANTIBODIES DIRECTED TO PGDF AND USES THEREOF  
Corvalan et al  
Appl. No.: 10/041,860  
Art Doc#: ABGENUX.051A

				#n.
1.6.1	A30	-3	TTAACCC (SEQ ID NO:116)	0 0 JK4 0
1.6.2	A30	-3	TTAACCC (SEQ ID NO:116)	0 0 JK4 0
1.6.3	A30	-3	TTAACCC (SEQ ID NO:116)	0 0 JK4 0
1.11.1	A3/119/DPK	-4	AAACTC (SEQ ID NO:118)	0 0 JK4 -2
1.11.2	A3/119/DPK	-4	AAACTC (SEQ ID NO:118)	0 0 JK4 -2
1.23.1	A30	-3	TTAACCC (SEQ ID NO:120)	0 0 JK1. 0
1.23.2	A30	-3	TTAACCC (SEQ ID NO:120)	0 0 JK1. 0



Clone #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.17.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D6-18	6	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D6-18	6	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.17.3	DP-50/3-33	0	GAGAGA (SEQ ID NO:121)	4	TCAA	D6-18	6	GGATACA (SEQ ID NO:122)	9	ATATGCTG G (SEQ ID NO:123)	JH6B	-1	TTACTACT (SEQ ID NO:124)
1.18	DP-15/1-8	1	CGAGAG (SEQ ID NO:125)	1	A	D6-19	19	GGGTATAG CAGTGCT GG (SEQ ID NO:126)	4	GAAG CTACTAC AC (SEQ ID NO:127)	JH6B	-2	TACTAC (SEQ ID NO:127)
1.24.1	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.24.2	DP-50/3-33	0	GAGAGA (SEQ ID NO:128)	4	TCAG	DK4	18	GGATACAG CTATGGTT AC (SEQ ID NO:129)	2	GT	JH6B	-4	CTACTA (SEQ ID NO:130)
1.25.1	DP-73/5-61	0	GAGACA (SEQ ID NO:131)	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATTAA TGGTTCCG AGACTTAA ATAA	3	TGT	JH4B	-4	CITTGAA (SEQ ID NO:135)

Figure 43A

ANTIBODIES DIRECTED TO PGDF AND USES THEREOF  
Carvalho et al.  
Appl. No.: 10/041,860 Arby Doctor: ABGENEX/051A



Clone #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.26.2	DP-73/5-61	0	GAGACA	6	TGGATC (SEQ ID NO:132)	D3-10	30	GTATATTAA TGTTTCGAG ACATTATT ATAA (SEQ ID NO:133)	3	TGT	JH4B	4	CITTTGA (SEQ ID NO:134)
1.29	DP-73/6-61	0	GAGACA	1	C	D5-12	21	GTGGATGT AGGGCT ACGATT (SEQ ID NO:136)	7	GGGGAT	JH6B	0	ATTACTAC (SEQ ID NO:138)
1.33	DP-14/1-18	0	GAGAGA	2	TC	D21-9	18	ATTACAT GATAGTAG TG (SEQ ID NO:140)	7	ATTATCT (SEQ ID NO:141)	JH6B	4	CITACTA (SEQ ID NO:142)
1.38.1	DP-50/3-33	1	CGAGAG	2	GA	D21-9	19	TATTACAT TGATAGTA GTG (SEQ ID NO:144)	7	ATTATCT (SEQ ID NO:145)	JH6B	4	CITACTA (SEQ ID NO:146)
1.38.1	DP-73/6-61	0	GAGACA	6	TGGATC (SEQ ID NO:147)	D3-10	31	GTATATTCA ATATTTCG GGGAGTTA TATAAC (SEQ ID NO:149)	2	GT	JH4B	4	CITTTGA (SEQ ID NO:150)
1.39.2	DP-73/6-61	0	GAGACA	6	TGGATC (SEQ ID NO:148)	D3-10	31	GTATATTCA ATATTTCG GGGAGTTA TATAAC (SEQ ID NO:149)	2	GT	JH4B	4	CITTTGA (SEQ ID NO:150)

Figure 43B

Appl. No.: 10/041,860 Arby Doctor: ABGENIX OSIA  
 Cordeiro et al. CDR filed 05/10/2007  
 ANTIBODIES DIRECTED TO PDGF AND USES THEREOF



CLONE #	VH	#DEL	VH END	#N's	N Sequence	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment
1.46.1	DP-16/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGT AGCTGCTA (SEQ ID NO:152)	2	CA	JH6B	-3	ACTACT (SEQ ID NO:153)
1.46.2	DP-16/1-8	1	CGAGAG (SEQ ID NO:151)	0	0	D2	25	ATATTGTA GTGGTGT AGCTGCTA (SEQ ID NO:152)	2	CA	JH6B	-3	ACTACT (SEQ ID NO:156)
1.45	DP-16/1-8	0	GAGAGG (SEQ ID NO:154)	2	CA	DK4	20	GTGGATAC AGCTATGG TTAC (SEQ ID NO:155)	1	G	JH6B	-3	ACTACT (SEQ ID NO:159)
1.46.1	DP-16/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GT GTGGTGT GCTGCTAC (SEQ ID NO:158)	2	GG	JH6B	-3	ACTACT (SEQ ID NO:159)
1.46.2	DP-16/1-8	1	CGAGAG (SEQ ID NO:157)	0	0	D2	25	ATATTGTA GTGGTGT AGCTGCTA (SEQ ID NO:158)	2	GG	JH6B	-3	ACTACT (SEQ ID NO:159)
1.46.1	DP-14/1-18	1	CGAGAG (SEQ ID NO:160)	7	TGTTGAA (SEQ ID NO:161)	D21-9	20	TATTACTA TGATGTTA GTGGTTAT (SEQ ID NO:162)	1	T	JH4B	0	ACTACT (SEQ ID NO:163)
1.46.2	DP-14/1-18	1	CGAGAG	7	TGTTGAA	D21-9	20	TATTACTA	1	T	JH4B	0	ACTACT

Figure 43C

Appl. No.: 10/041,860 Atty Doctor: ABGENX,OSIA  
 Crowsden et al.  
 ANTIODIDES DIFFERENTED TO PDGF AND USES THEREOF



Clone #	VH	#DEL	VH END	#N's	N Sequence (SEQ ID NO:160)	DH	Size of D	D Sequence	# N's	N Sequence	JH	# del	JH Segment (SEQ ID NO:163)
								TGATGTAA GTGGTTAT (SEQ ID NO:162)					
1.48.1	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.49.2	DP-15/1-8	2	GCGAGA (SEQ ID NO:164)	5	ATGAG (SEQ ID NO:165)	D5-12	17	GGATATAG TGGCTACG A (SEQ ID NO:166)	3	GCT	JH6B	0	ATTACTAC (SEQ ID NO:167)
1.51.1	DP-73/5-51	0	GAGACA (SEQ ID NO:166)	1	C	D3-16	31	TATGATTA CCTTGGaa GGAAATT (SEQ ID NO:169)	6	CAGGG (SEQ ID NO:170)	JH5B	-5	TGGTTC (SEQ ID NO:171)
1.51.2	DP-73/5-51	0	GAGACA (SEQ ID NO:166)	1	C	D3-16	31	TATGATTA CCTTGGaa GGAAATT (SEQ ID NO:169)	6	CAGGG (SEQ ID NO:170)	JH6B	-5	TGGTTC (SEQ ID NO:171)

Figure 43D

ANTI-BODIES DIRECTED TO PGF/F AND USES THEREOF  
Crovold et al.  
Appl. No.: 10/041,860 Arny, Doctor; ABGENIX, OSAIA

Clone	VK	#del	VK end	#n	N SEQ	Jk	# del	Jk end
1.17.1	A30	3	TTACCC (SEQ ID NO:172)	0	0	JK4	0	GCTCACT (SEQ ID NO:173)



CLONE	VK	#del	VK end	#n	N SEQ	Jk	# del	Jk end
1.17.2	A30	3	TTACCC (SEQ ID NO:1.172)	0	0	JK4	0	GCTCACT (SEQ ID NO:1.73)
1.17.3	A30	3	TTACCC (SEQ ID NO:1.172)	0	0	JK4	0	GCTCACT (SEQ ID NO:1.73)
1.18	A30	3	TTACCC (SEQ ID NO:1.172)	0	0	JK3	0	ATTCAAC (SEQ ID NO:1.75)
1.24.1	A30	3	TTACCC (SEQ ID NO:1.176)	0	0	JK1	0	GTGGAC (SEQ ID NO:1.77)
1.24.2	A30	3	TTACCC (SEQ ID NO:1.176)	0	0	JK1	0	GT(GGAC (SEQ ID NO:1.77)
1.25.1	A30	3	TTACCC (SEQ ID NO:1.176)	0	0	JK1	0	GTGGAC (SEQ ID NO:1.77)
1.25.2	A30	3	TTACCC (SEQ ID NO:1.176)	0	0	JK1	0	GTGGAC (SEQ ID NO:1.77)
1.29	A3/A18/DPK	7	CTACAA (SEQ ID NO:1.180)	14	TCTCTCATG	JK2	-7	TTTGG (SEQ ID NO:1.62)
1.33	A20/DPK4	3	TGCCCG (SEQ ID NO:1.181)	0	0	JK4	0	GCTCAC (SEQ ID NO:1.64)
1.38.1	A20/DPK4	3	TGCCCG (SEQ ID NO:1.185)	0	0	JK1	0	GTGGAC (SEQ ID NO:1.66)
1.39.1	A30	3	TTACCC (SEQ ID NO:1.187)	0	0	JK1	0	GTGGAC (SEQ ID NO:1.68)

Figure 43E

ANTIBODIES DIRECTED TO PGDF AND USES THEREOF  
Corvalan et al.  
Appl. No.: 10/041,860 Atty. Doctor: ABGENIX/OSIA



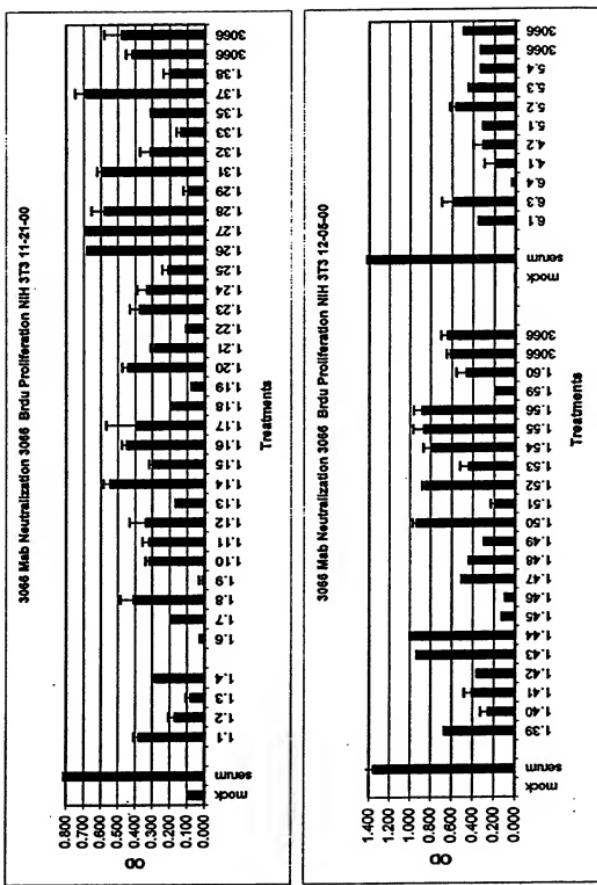
CLONE	VK	#del	VK end	#n	N SEQ	JK	# del	JK end
1.38.2	A30	3	TGACCC (SEQ ID NO:1.87)	0	0	JK1	0	GTTGGAC (SEQ ID NO:1.88)
1.46	A20/DPK4	3	TGCCCC (SEQ ID NO:1.89)	0	0	JK3	0	ATTGAC (SEQ ID NO:1.90)
1.46.1	A30	0	CCCTCC (SEQ ID NO:1.91)	0	0	JK1	-3	GACGTT (SEQ ID NO:1.92)
1.46.2	A30	0	CCCTC (SEQ ID NO:1.91)	0	0	JK1	-3	GACGTT (SEQ ID NO:1.92)
1.48.1	L6/DPK5/V	1	TCCC (SEQ ID NO:1.93)	0	0	JK1	-2	GGAGGT (SEQ ID NO:1.94)
1.48.2	L6/DPK5/V	1	TCCC (SEQ ID NO:1.93)	0	0	JK1	-2	GGAGGT (SEQ ID NO:1.94)
1.49.1	A3/A19/DPK	5	CAAACCT (SEQ ID NO:1.95)	0	0	JK5	-1	ATCACCC (SEQ ID NO:1.96)
1.49.2	A3/A19/DPK	6	CAAACCT (SEQ ID NO:1.95)	0	0	JK5	-1	ATCACCC (SEQ ID NO:1.96)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:1.97)	1	T	JK3	0	ATTCAAC (SEQ ID NO:1.98)
1.51.1	A27/A27A	4	GCTCAC (SEQ ID NO:1.97)	1	T	JK3	0	ATTCAAC (SEQ ID NO:1.98)

Figure 43F

Appl. No.: 10/041,860 Atty Doc#: ABGENX.051a  
 Corvelan et al.  
 ANTBODIES DIFFERED TO PDGF AND USES THEREOF



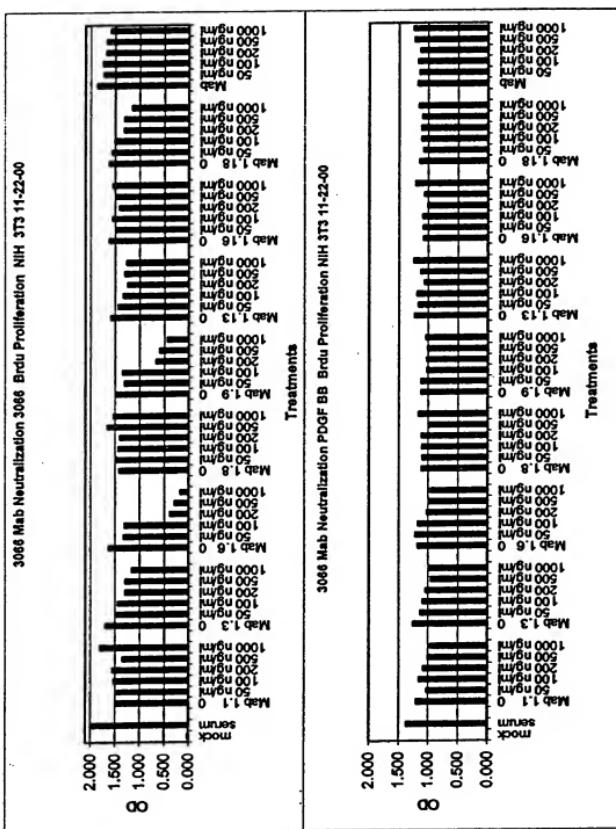
FIGURE 44



Appl. No.: 10/041,860 Att'y Doctor: ABGENIX,OSIA  
Corradini et al.  
ANTIBODIES DIRECTED TO PDGF AND USES THEREOF

Aug 13 2002 EJC  
PATENT STAMP

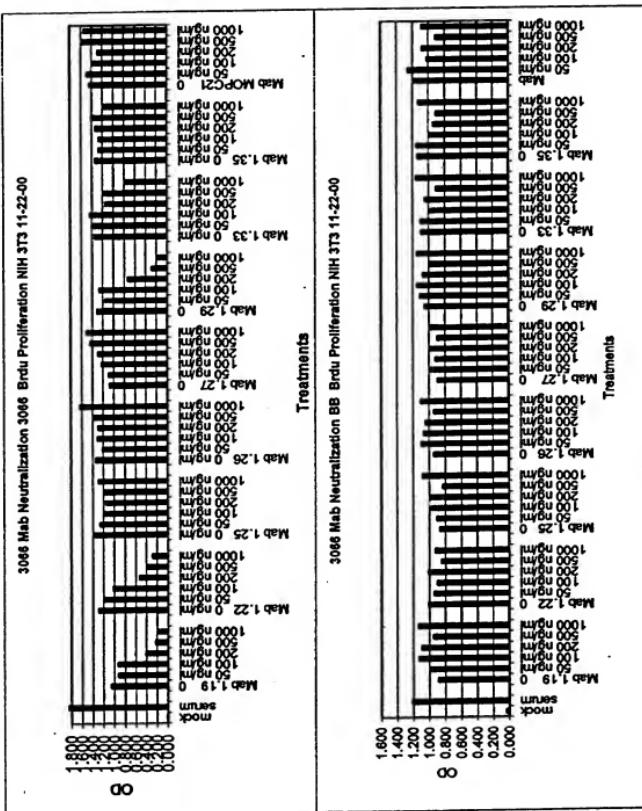
**FIGURE 45**



ANTIBODIES DIRECTED TO PDGF AND USES THEREOF  
Corvalan et al.  
Appl. No.: 10/041,860 Arly Docket: ABGENX-051A



**FIGURE 46**



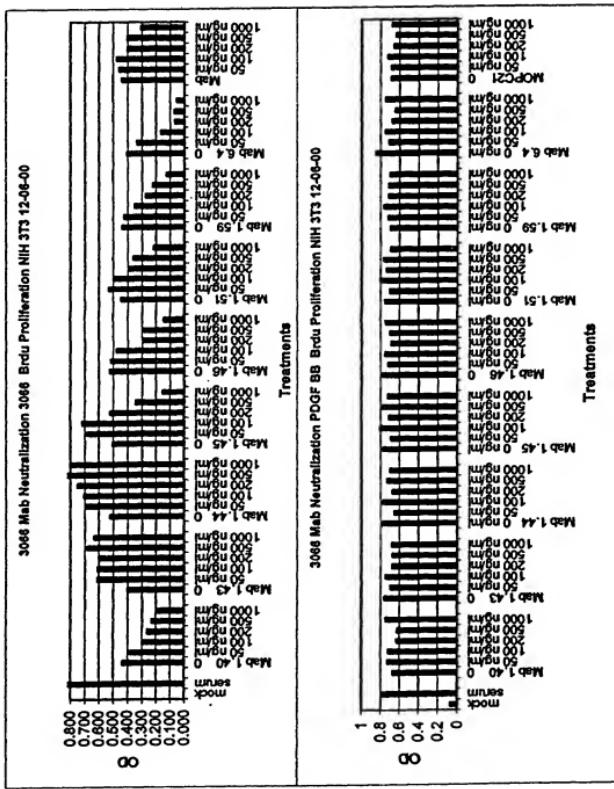
App. No.: 10/041,860 Amy Docket: ABGENRAU31A

Corvalan et al.

ANTIBODIES DIRECTED TO PDGF AND USES THEREOF



**FIGURE 47**



ANTIBODIES DIRECTED TO PDGF AND USES THEREOF  
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Appl. No.: 10/041,860 Arny Doctor: ABGENIX/OSIA

PATENT  
 AUG 13 2002

FIGURE 48

1.19 H 1 Q	A	A V V K	T	D N	T Q	WMNPNSGN G 60
6.4 H 1 O	A	A V V K	T	D N	T Q	WINPNSGN D 60
1.18 H 1 Q	A	A V V K	T	D N	T Q	WMNPNSGN G 60
1.40 H 1 Q	A	A V V K	T	T D N	T Q	WMNPNSGN G 60
1.45 H 1 Q	A	A V V K	T	D N	T Q	WMNPNSGN G 60
1.46 H 1 Q	A	A V V K	S	D N	T Q	WMNPNNGN G 60
1.49 H 1 Q	A	A V V K	T	D N	T Q	WMNPNSGD G 60
1.33 H 1 Q	A	A V V K	T	G S	P Q	WISAYNGN N 60
1.48 H 1 Q	A	A V V K	T	G S	P Q	WISAYNGN N 60
1.6 H 1 E	E GGLV	G LRL A	FN RT	NNM	P K	VSSISSSSNIY 60
1.17 H 1 Q	E GG VQ	K LRL A	FT S	GMH	P K	VAVIYDGGNSKY 60
1.24 H 1 Q	E GG VQ	R LRL A	FS S	GMH	P K	VADIYDGGNSKY 60
1.38 H 1 Q	E GG VQ	R LRL A	FT S	GMH	P K	VAIIVYDGNKY 60
1.11 H 1 E	GGLIQ	G LRL A	FTVS	NYMS	P K	VSVIYSGGS Y 59
1.23 H 1 E	A	E L I EG	S	W G	MP K	IIYPGDSD R 60
1.25 H 1 E	A	E L I KG	R	W G	MP K	IIYPGDSD R 60
1.29 H 1 E	A	E L I KG	S	W G	MP K	IIYPGDSD R 60
1.39 H 1 E	T	E L I KG	R	W G	MP K	IIYPGDSD R 60
1.51 H 1 E	A	E L I KG	S	W G	MP K	IIYPGDSDAK 60

[ CDR1 ]

[ CDR2 ]

1.19 H 61 QKF	V MTRNT I	MELS	SE	I	--DVM-ITFGGVIVH-YGM V	116
6.4 H 61 QKF	V MTRDT I	MELS	SE	V	--GPG-YSYN-YD -YGM V	115
1.18 H 61 QKF	V MTRNT I	MELS	SE	V	--EG-IAVAGTV YYGN V	116
1.40 H 61 QKF	V MTRNT L	MELS	SE	V	--DIV-VVVAATN -NGN V	116
1.45 H 61 QKF	V MTRNT I	MELS	SE	V	--GSG-YSYG-YD -YGM V	115
1.46 H 61 QKF	V MTRNT I	MELS	SE	V	--DIV-VVVATAD -YGM V	116
1.49 H 61 QKF	V MTRNT I	MELS	SE	V F	--MRD-IVATSYY FYGM V	117
1.33 H 61 QKL	V MTTDT T	MELR	SD	V	--DHY-YDSSDYL YYGL V	117
1.48 H 61 QKL	V MTTDT T	MELR	SD	V	--DVEYY-YDGSGYY FDY---	115
1.6 H 61 DSVK	F ISRDNAKNSL	LQMN	AE	V	DIMI---TFG-GIASEFY Y	116
1.17 H 61 DSVK	F ISRDN KN L	LQMN	AE	V	DQGY---RYA-GY DYGM V	116
1.24 H 61 DSVK	F ISRDN KN L	LQMN	AE	V	DQGY---SYG-YV DYGM V	116
1.38 H 61 DSVK	F VSRDN KN L	LQMN	AE	V	GYYYD-SSD-YL YYGN V	117
1.11 H 60 DSVK	F ISRDN KN L	LQMN	AE	V	GTVT-----N YYGN V	110
1.23 H 61 SPF	QV ISADK I	LQWS	KAS	M	HVSY---YYVSGS -NVF Y	116
1.25 H 61 SPF	QV ISADK I	LQWS	KAS	M	HGSY---YYGSET -NVF Y	116
1.29 H 61 SPF	QA ISADK I	LQWS	KAS	M	HVDVGATIGGYYY -HGM V	119
1.39 H 61 SPF	QV ISADK I	LQWS	KAS	M	HGSY---YYNSGS -NVF Y	116
1.51 H 61 SPF	QV ISADK I	LQWS	KAS	M	HYDY---VWRNR T-GWF P	116

[ CDR3 ]



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FIGURE 48 (CONT)

1.19	H	117	T	126
6.4	H	116	T	125
1.18	H	117	T	126
1.40	H	117	T	126
1.45	H	116	T	125
1.46	H	117	T	126
1.49	H	118	T	127
1.33	H	118	T	127
1.48	H	116	L	125
1.6	H	117	L	126
1.17	H	117	T	126
1.24	H	117	T	126
1.38	H	118	T	127
1.11	H	111	T	120
1.23	H	117	L	126
1.25	H	117	L	126
1.29	H	120	T	129
1.39	H	117	L	126
1.51	H	117	L	126

AUG 13 2002  
J.C.  
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FIGURE 49

1.48 L 1	V	T	SS-----W A	A KL	I Q 55
1.49 L 1	V	L PVT P EPAS S S	SLLHSNGNY D LL	QS QL	LG SRA 60
1.11 L 1	V	L PVT P EPAS S S	SLLQSNGNY D L	QS QL	LG NRA 60
1.29 L 1	V	L PVT P EPAS S S	SLLHSNGNY D L	QS QL	LG NRA 60
1.45 L 1		N	SN-----D A	V KL	T Q 55
1.33 L 1		T	SN-----Y A	V KL	T Q 55
1.38 L 1		T	SN-----Y A	V NL	T Q 55
6.4 L 1	E VL	GT L P E A LS	SVSSS----Y A	QA RL	T SRA 56
1.51 L 1	E VL	GT L P E A LS	SVSSS----Y A	QA RL	G NRA 56
1.19 L 1		T	RN-----D G	A KR	S Q 55
1.18 L 1		T	RN-----D G	A KR	S Q 55
1.16 L 1		T	RN-----D G F	A KR	S Q 55
1.23 L 1		T	RN-----D G	I A KR	S Q 55
1.25 L 1		T	RN-----D G	A KR	S Q 55
1.39 L 1		T	RN-----D G	A KR	S Q 55
1.17 L 1		T	RN-----D G	A KR	S Q 55
1.24 L 1		T	RN-----D G	A KR	S Q 55
1.46 L 1		T	RN-----D G	A KR	F S P 55
			[ CDR1 ]		[ CDR2 ]

1.48 L 56	D	F S	Q SN F R -	Q	107
1.49 L 61	D	D K RVEA VGV	M TLQTIT--	Q RL	111
1.11 L 61	D	D K RVEA VGV	M ALQTLT--	G	111
1.29 L 61	D	D K RVEAD VGV	M ALQSLMCS	Q L	113
1.45 L 56	L	D	V T QKYN A F -	P D	107
1.33 L 56		D	V T QKYN A L -	G	107
1.38 L 56		D S	V A QKCN A W -	Q T	107
6.4 L 57	T I D	D D	R E F V Q YG S CS-	Q L	108
1.51 L 57	T I D	D D	R E F V Q YG SLF -	P D	108
1.19 L 56		D	F T L HN D CS-	Q L R	107
1.18 L 56		E	F T F L HN Y F -	P D	107
1.16 L 56		E	F T L HN Y L -	G	107
1.23 L 56	R	E	F T L HN Y W -	Q	107
1.25 L 56		E	F T L HN Y W -	Q	107
1.39 L 56		E	F T L HN Y W -	Q	107
1.17 L 56		E	F T L HN Y L -	G	107
1.24 L 56		E	F T L HN Y W -	Q	107
1.46 L 56		E	F T L HSGY P -	Q	107
			[ CDR3 ]		



10044860 .081302  
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Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 50

1.19 H 1			I	D	60
6.4 H 1					60
1.18 H 1					60
1.40 H 1			T		60
1.45 H 1					60
1.46 H 1			S		60
1.49 H 1				N	60
				D	60
		[ CDR1 ]		[ CDR2 ]	
1.19 H 61					119
6.4 H 61	D		I	V	118
1.18 H 61				GFGYSYN--YD	119
1.40 H 61	L			EGIAVAGT--YY	119
1.45 H 61				DIVVVVAA-TN N	119
1.46 H 61				GSSGYSYG--YD	118
1.49 H 61	F			DIVVVVTA-TD	119
				MRDIVATSYYY F	120
				[ CDR3 ]	
1.19 H 120		126			
6.4 H 119		125			
1.18 H 120		126			
1.40 H 120		126			
1.45 H 119		125			
1.46 H 120		126			
1.49 H 121		127			



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FIGURE 51

1.33 H 1  
1.48 H 1

60

60

[ CDR1 ]

[ CDR2 ]

1.33 H 61  
1.48 H 61

--DH S D L YY GLDV 118  
DVEY G G Y FD ---- 116  
[ CDR3 ]

1.33 H 119 T 127  
1.48 H 117 L 125



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10041860-081302

FIGURE 52

1.17 H 1	K	T	V	SN	60
1.24 H 1	R	S	D	SN	60
1.38 H 1	R	T	I	ND	60
		[ CDR1 ]		[ CDR2 ]	

1.17 H 61	I	DQG -RYAGY	D	119
1.24 H 61	I	DQG -SYGYV	D	119
1.38 H 61	V	GYY DSSDYL	Y	120
		[ CDR3 ]		

1.17 H 120	126
1.24 H 120	126
1.38 H 121	127



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Appl. No.: 10/041,860 Atty Docket: ABGENIX.051A

FIGURE 53

1.23 H 1	E	S	60
1.25 H 1		R	60
1.29 H 1		S	60
1.39 H 1	T	R	60
1.51 H 1		S	AK 60

[ CDR1 ]

[ CDR2 ]

1.23 H 61	VS YYVSG---S NV Y 117
1.25 H 61	GS YYGSE---T NV Y 117
1.29 H 61	VDVGATIGGYY HGM V 120
1.39 H 61	GS YYNSG---S NV Y 117
1.51 H 61	YD VWRNY---R TGW P 117

[ CDR3 ]

1.23 H 118	126
1.25 H 118	126
1.29 H 121 T	129
1.39 H 118	126
1.51 H 118	126



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FIGURE 54

1.49 L 1  
1.11 L 1  
1.29 L 1

H	L	S 60
Q	Q	N 60
H	Q	N 60
[ CDR1 ]		[ CDR2 ]

1.49 L 61  
1.11 L 61  
1.29 L 61

]

E	T	TIT--	Q	RL	111
E	A	TLT--	G	KV	111
D	A	SLMCS	Q	KL	113
[ CDR3 ]					



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FIGURE 55

1.45 L 1  
1.33 L 1  
1.38 L 1

N	D	K	L	60
T	Y	K	S	60
T	Y	N	S	60

[ CDR1 ] [ CDR2 ]

1.45 L 61  
1.33 L 61  
1.38 L 61

T	T	Y	F	P	K	D	107
T	T	Y	L	G	K	E	107
S	A	C	W	Q	T	E	107

[ CDR3 ]

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Appl. No.: 10/041,860 Atty Docket: ABGENIX 051A

FIGURE 56

6.4 L 1  
1.51 L 1

AT S 60  
GA N 60  
[ CDR1 ]

6.4 L 61  
1.51 L 61

PCS Q LE 108  
LFT P VD 108  
[ CDR3 ]



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10041860 .081302

FIGURE 57

1.19 L 1							60
1.18 L 1							60
1.16 L 1							60
1.23 L 1				F			60
1.25 L 1					I		60
1.39 L 1						R	60
1.17 L 1							60
1.24 L 1							60
1.46 L 1							60
						F	60
						P	60

[ CDR1 ]

[ CDR2 ]

1.19 L 61	D			D	CS	Q	L	R	107
1.18 L 61				F	F	P	D		107
1.16 L 61					L	G			107
1.23 L 61					W	Q			107
1.25 L 61					W	Q			107
1.39 L 61					W	Q			107
1.17 L 61					L	G			107
1.24 L 61					W	Q			107
1.46 L 61					SG	P	Q		107

[ CDR3 ]